DESCRIPTION

INSULATED HERPESVIRUS-DERIVED GENE EXPRESSION CASSETTES FOR SUSTAINED AND REGULATABLE GENE EXPRESSION

1.0 BACKGROUND OF THE INVENTION

The present application claims priority to United States Provisional Application Serial No. 60/545,375, filed February 17, 2004, the entire contents of which is specifically incorporated herein by reference in its entirety. The United States government has certain rights in the present invention pursuant to NIAID grant R01-AI48633 from the National Institutes of Health.

1.1 FIELD OF THE INVENTION

The present invention relates generally to the fields of molecular biology and virology, and in particular, to genetic expression cassettes, and vector comprising them useful for the delivery of nucleic acid segments encoding selected therapeutic constructs (including for example, peptides, polypeptides, ribozymes, and catalytic RNA molecules), to selected cells and tissues of vertebrate animals. In particular, these genetic constructs are useful in the development of gene therapy vectors, including for example, HSV, AV, and AAV vectors, for the treatment of mammalian, and in particular, human diseases, disorders, and dysfunctions. The disclosed compositions may be utilized in a variety of investigative, diagnostic and therapeutic regimens, including the prevention and treatment of a variety of human diseases. Methods and compositions are provided for preparing viral vector compositions comprising these genetic expression cassettes for use in the preparation of medicaments useful in central and targeted gene therapy of diseases, disorders, and dysfunctions in an animal, and in humans in particular.

1.2 DESCRIPTION OF THE RELATED ART

Currently, viral vectors show the greatest efficiency in gene transfer (reviewed in Anderson, 1998; Verma and Somia, Nature, 1997). For correction of genetic diseases such that persistent gene expression is required, herpesvirus, retrovirus, lentivirus, adenovirus, or AAV based vectors are desirable due to the integrating nature of the viral life cycle.

In considering transgene expression, there are many known situations where a transferred gene(s) is capable of a short period of expression however followed by a decline to undetectable levels without the loss of the expression construct. These expression constructs may sustain transgene expression for periods of time up to 2 weeks and on rare occasions 2 months (Palmer *et al.*, 2000). Unfortunately, despite claims of sustained expression up to 2 months, the over-ruling factor is that one can anticipate an eventual decline of transcript levels often to near zero levels. As a result, this presents an additional variable to transgene expression; the predictability or probability of transgene

expression. For the purposes of gene therapy, transgene expression kinetics must be predictable to achieve safe and reliable therapeutic effects.

The mechanisms responsible for transcript loss have been attributed to elaborate defense mechanisms used by eukaryotic cells to protect both the structure of their genomes and to oppose expression of abnormal transcription units (Bestor, 2000). These mechanisms include, but are not limited to, DNA methylation, multi-copy repeat-induced transgene silencing, post-transcriptional gene silencing (PTGS) mediated by RNAi, position effects that impose histone methylation/deacetylation. These host defense mechanisms represent a formidable barrier to many forms of gene therapy. Current gene therapy applications often depend on a construct or recombinant virus with the ability to express an agent of interest (protein or RNA) in a particular tissue. However, cells can detect alterations within their genome due to multi-copy transgene insertions or to abnormal transcripts and elicit a strong and heritable silencing effect. A common example of multi-copy transgene silencing is in the generation of transgenic animals. It had previously been found that transgene copy number was inversely proportional to the level of gene expression in some lines of transgenic mice. It is thought that end-to-end ligation of the expression construct and/or homologous recombination between construct molecules generates transgene concatemers (often 5-50 copies) that integrate at a single site within the genome (Dobie *et al.*, 1997). Unfortunately, the tandem repeats appear to contribute to a phenomenon similar to position effect varigation (PEV). PEV may be the result of position-dependent inactivation of the expression construct mediated by the surrounding heterochromatin environment and results in the heritable maintenance of the transcription "off" state (Dobie *et al.*, 1997).

2.0 SUMMARY OF THE INVENTION

The present invention overcomes limitations inherent in the prior art by providing genetic constructs comprising nucleic acid sequences derived from Herpes Simplex Virus type I (HSV-I) that are capable of facilitating persistent/long-term and regulatable transgene expression in selected host cells. An important feature of these new gene expression cassettes is that the cassette is bounded by control elements that protect and insulate the gene expression portion of the cassette from the influence of DNA and chromatin structure that lie outside of the cassette, when the cassette is inserted into a viral vector or a cellular genome. These control elements effectively maintain the expression cassette in an accessible and transcriptionally-responsive conformation. The expression cassettes of the present invention facilitate predictable and sustained expression of a transgene regardless of where the cassette was inserted. For example, the cassette may be used to insert a transgene into a viral vector (including, for example, but not limited to adenovirus, adeno-associated virus (AAV), retrovirus (Lentivirus), or Herpesviruses), or into the genome of a eukaryotic cell, including mammalian cells such as human cells.

Following appropriate delivery or insertion of the genetic constructs into suitable recipient cells, the cassette is specifically engineered to express a gene of interest in a regulated manner for the duration of the cell's life. Importantly, this invention addresses a common and presently intractable problem associated with the failure of many gene therapy vectors or transgenic animals to express genes at predictable and sustained levels due to the repressive effects of the surrounding chromatin.

Another important aspect of the present invention is that by employing selected control elements within the genetic constructs that contain particular nucleic acid sequences, it is possible to confer cell-type specific expression. For example, in an illustrative embodiment, the expression cassette may contain the components from HSV-1 that allow regulation of the control elements in neurons. By modifying these elements, however, one may alter the cell type and tissue specificity to allow the cassette to function in other cell types such as, for example, in the liver or in lung tissue.

In one embodiment, the cassette employs a defective form of HSV-1 vector as the vehicle to carry the gene expression cassette for *ex vivo* gene transfer to the central and peripheral nervous systems. This illustrative delivery system comprises two parts: (1) the insulated gene expression cassette and (2) a defective HSV-I based virus vector to deliver the transgene to the CNS. The ability of this cassette to maintain persistent, long-term gene expression, in a highly regulated manner, represents a powerful tool in the fields of gene therapy, basic gene expression assays, and in the development of animal disease models.

In one embodiment, the invention provides an isolated polynucleotide that comprises at least a first isolated HSV LAT enhancer element, at least a first isolated LAT insulator/boundary region operably positioned upstream of the isolated LAT enhancer element, and at least a second isolated LAT insulatory/boundary region operably positioned downstream of the isolated LAT enhancer element. The LAT enhancer element may comprise, consist essentially of, or consist of a contiguous nucleotide sequence from an HSV LAT 5′ exon. In preferred embodiments, the LAT enhancer element may comprise, consist essentially of, or consist of, a contiguous nucleotide sequence from about nucleotide 118,975 to about nucloetide 120,471 of an HSV LAT 5′ exon, or more preferably a contiguous nucleotide sequence from about nucleotide 118,975 to about nucloetide 120,471 of an HSV LAT 5′ exon, or more preferably still, a contiguous nucleotide sequence from about nucleotide 118,975 to about nucloetide 120,471 of an HSV LAT 5′ exon. In certain embodiments, an even smaller LAT enhancer element may be preferred, and in such conditions, the enhancer element may comprise, consist essentially of, or consist of, a contiguous nucleotide sequence from about nucleotide 118,975 to about nucloetide 120,471 of an HSV LAT 5′ exon. Exemplary human HSV genomes have been illustrated in SEQ ID NO:109, SEQ ID NO:110, and SEQ ID NO:111, which represent the complete genomic sequences of the human HSV 1, 2, and 3 virus, respectively.

In certain embodiments, the isolated expression cassettes of the invention may, in addition to the polynucleotides described above, further comprise a nucleic acid segment that comprises at least a first promoter region operably positioned upstream of the LAT enhancer element, and downstream of the first LAT insulator/boundary region. Exemplary promoter regions include, but are not limited to, an HSV LAP1 promoter. In certain embodiments, the HSV LAP1 promoter comprises, consists essentially of, or consists of, a sequence region of from about nucleotide 117,938 to about 118,843 of the HSV genome.

The first LAT insulator/boundary region of the disclosed expression cassette, may comprise, consist essentially of, or consist of, a contiguous nucleotide sequence from an HSV insulator region or an HSV boundary region. Exemplary sequences for such a first LAT insulator/boundary region include sequence regions that comprise, consist essentially of, or consist of, a contiguous nucleotide sequence from about nucleotide 8365 to about nucleotide 9273 of the human HSV genome, and in particular, from the HSV 1 genome as identified in SEQ ID NO:109.

The second LAT insulator/boundary region of the disclosed expression cassette may comprise, consist essentially of, or consist of, a contiguous nucleotide sequence from an HSV insulator region or an HSV boundary region. Exemplary sequences for such a second LAT insulator/boundary region include sequence regions that comprise, consist essentially of, or consist of a contiguous nucleotide sequence from about nucleotide 120,208 to about nucleotide 120,940 of the human HSV genome, and in particular, from the HSV 1 genome as identified in SEQ ID NO:109.

The disclosed polynucleotides may also optionally further comprise at least a first multiple cloning region operably positioned downstream of the first LAT insulator/boundary region and upstream of the LAT enhancer element. This multiple cloning region may also further comprise a nucleic acid sequence that encodes at least a first promoter or at least a first enhancer sequence that can be used to express a selected gene operably placed under its control in a suitable mammalian host cell.

The disclosed polynucleotides may also optionally further comprise at least a second multiple cloning region operably positioned upstream of the second LAT insulator/boundary region and downstream of the LAT enhancer element. This second multiple cloning region may also optionally further comprises at least a first nucleic acid sequence that encodes a heterologous peptide, polypeptide, or enzyme, and preferably, one that encodes a heterologous therapeutic agent, including for example, antibodies, antigen binding domains, peptides, polypeptides, enzymes, ribozymes, or even antisense polynucleotides.

Exemplary therapeutic agents include, but are not limited to, peptides or polypeptides such as an antibody, a growth factor, a neurotrophic factor, a transcription factor, an anti-apoptotic factor, a proliferation factor, an enzyme, a cytotoxin, a transcription factor, an apoptotic factor, a tumor suppressor, a kinase, a cytokine, a lymphokine, a protease, or other therapeutic polypeptide that may be beneficial when expressed in a mammalian host cell.

When it is desirable to express two or more therapeutic agents in a host cell, the second multiple cloning region may also optionally further comprise at least a second distinct nucleic acid sequence that encodes at least a second distinct therapeutic agent. As in the case of the first therapeutic agent, the second agent may also be selected from the group consisting of a peptide, an antibody, a protein, a polypeptide, a ribozyme, a catalytic RNA molecule, an antisense oligonucleotide, and an antisense polynucleotide.

When a catalytic RNA molecule is selected as the therapeutic agent, this ribozyme will preferentially and specifically cleave a first mRNA molecule encoding, for example, a transcription factor, an anti-apoptotic factor, an enzyme, a proliferation factor, a receptor, a growth factor, an oncogenic peptide, a signaling polypeptide, or a growth factor polypeptide. Exemplary catalytic RNA molecules include, for example, hammerhead and hairpin ribozymes.

The expression cassettes of the invention typically will be on the order of about 1000 to about 10,000 nucleotides in length, and more preferably, of from about 2000 to about 9000 nucleotides in length, or of from about 3000 to about 8000 nucleotides in length, of from about 4000 to about 7000 nucleotides in length, although larger or smaller expression cassettes are contemplated to be useful in certain embodiments.

Another embodiment of the invention concerns vectors that comprise one or more of the disclosed expression cassette polynucleotides. Exemplary vectors include plasmids, with one such vector, Insulated Viral Artificial Chromosome vectors (IVACs) being particularly preferred. In illustrative embodiments, one such plasmid vector is described in detail hereinbelow and show in FIG. 12A and FIG. 12B. This vector has been designated pIVAC_1.0.

Another embodiment of the invention concerns viral vectors, virions, or viral particles that comprise one or more of the disclosed expression cassette polynucleotides. Such vectors will preferably comprise a retroviral, adenoviral, adeno-associated viral, or a herpes viral vector. Exemplary vectors include gutless HSV vectors, gutless AV vectors, gutless AAV vectors, recombinant HSV vectors, recombinant AV vectors, and recombinant AAV vectors that comprise, consist essentially of, or consist of, one or more of the disclosed expression cassettes. Pluralities of such viral particles, as well as host cells comprising them also represent important embodiments of the invention. Preferred host cells include animal cells, with mammalian host cells, and human host cells in particular, being preferred.

The compositions of the present invention when used in therapy of mammals, and in therapy of humans in particular, may also further optionally comprise one or more pharmaceutical excipients, diluents, buffers, or such like, and may optionally further comprise a lipid, a liposome, a lipofection complex, a nanoparticle, a nanocapsule, or other component to facilitate improved cellular adhesion, infection, or uptake. Preferably compositions of the present invention will be formulated with

pharmaceutical excipients that are designed for administration to a human host cell through suitable means, such as injection.

In another embodiment, the invention concerns therapeutic, diagnostic, and prophylactic kits. Such kits are often suitable for commercial sale, and typically will comprise in suitable container means: (a) one or more components polynucleotides, plasmid vectors, viral vectors, virions, or viral particles, host cells, or compositions that comprise them; and (b) instructions for using the kit.

In another embodiment, the invention concerns the use of the polynucleotides, expression cassettes, viral vectors, and compositions comprising them in the manufacture of medicaments and in methods for treating, preventing, or ameliorating the symptoms of a disease, disorder, defect, or dysfunction in an animal, preferably mammals, and in particular, humans. Such polynucleotides and expression vectors are contemplated to be particularly useful in the manufacture of medicaments and in methods for preventing, treating, or alleviating the symptoms of one or more mammalian diseases, including, but not limited to, cancer, diabetes, autoimmune disease, kidney disease, cardiovascular disease, pancreatic disease, liver disease, cystic fibrosis, muscular dystrophy, neurological disease, neurosensory dysfunction, stroke, ischemia, an enzyme deficiency, a psychological deficit, a neuromuscular disorder, an eating disorder, a neurological deficit or disease, a neuroskeletal impairment or disability, Alzheimer's disease, Huntington's disease, Parkinson's disease, pulmonary disease, a skin disorder, a burn, or a wound, or such like. The vectors and pharmaceutical compositions of the invention are also contemplated to find utility in the manufacture of medicaments and methods for administering genetic constructs to selected human cells for use in various treatment modalities, including for example, *ex vivo*, *in situ*, *in vitro*, or *in vivo* gene delivery. The use of such compositions in the development of viral gene therapy vectors, such as recombinant AV, AAV, and/or HSV vectors, is particularly envisioned by the present inventors.

3.0 BRIEF DESCRIPTION OF THE DRAWINGS

The following drawings form part of the present specification and are included to further demonstrate certain aspects of the present invention. The invention may be better understood by reference to the following description taken in conjunction with the accompanying drawings, in which like reference numerals identify like elements, and in which:

FIG. 1 shows an illustrative gene expression cassette of the present invention. The therapeutic gene of interest may be cloned into the multiple cloning site 3' of the LAT enhancer, while the MCS upstream of the LAT promoter may be utilized to facilitate introduction of one or more additional promoter elements for expression of the selected gene of interest. HSV type I strain 17syn+ neuronal-specific DNA boundary element; Cell-type specific boundary elements may be swapped in/out. HSV type I strain 17syn+ insulator element capable of protecting and maintaining the gene expression portion of the cassette in highly responsive transcriptional state. Multiple cloning sites represented by

a cluster of restriction enzyme sites that may be used to facilitate cloning of the gene of interest and/or an additional promoter element. HSV type I strain 17syn+ latency associated transcript (LAT) core promoter. HSV type I strain 17syn+ latency associated transcript (LAT) 5' exon DNA exhibiting enhancer function. The element is bound by Splice Donor (SD) and Splice Acceptor (SA) sites to facilitate splicing of the transcript's 'artificial' intron from the desired downstream gene of interest transcript. Splicing also promotes nuclear export of desired transcript.

FIG. 2 shows another an illustrative gene expression cassette of the present invention. The therapeutic gene of interest may be cloned into the multiple cloning site 3' of the LAT enhancer, while the MCS upstream of the LAT promoter may be utilized to facilitate introduction of one or more additional promoter elements for expression of the selected gene of interest. HSV type I strain 17syn+ neuronal-specific DNA boundary element; Cell-type specific boundary elements may be swapped in/out. HSV type I strain 17syn+ insulator element capable of protecting and maintaining the gene expression portion of the cassette in highly responsive transcriptional state. Multiple cloning sites represented by a cluster of restriction enzyme sites that may be used to facilitate cloning of the gene of interest and/or an additional promoter element. HSV type I strain 17syn+ latency associated transcript (LAT) core promoter. HSV type I strain 17syn+ latency associated transcript (LAT) 5' exon DNA exhibiting enhancer function. The element is bound by Splice Donor (SD) and Splice Acceptor (SA) sites to facilitate splicing of the transcript's 'artificial' intron from the desired downstream gene of interest transcript. Splicing also promotes nuclear export of desired transcript. Transcriptionally repressed regions of DNA located outside of the insulated cassette.

FIG. 3A, **FIG. 3B** and **FIG. 3C** show titers of infectious virus detected in eye swabs, corneas, and TG during acute infections following inoculation with high and low doses of LAT^+ and LAT^- viruses. Rabbits were inoculated with 500,000 or 500 PFU of either 17ΔPst (LAT^-) or 17ΔPstR (LAT^+). At the indicated times, eye swabs were taken, the rabbits were sacrificed, and corneas and TG were dissected. Virus titers were determined by standard plaque assays and are expressed as the log titer of infectious virus present in the eye swabs (FIG. 3A), corneas (FIG. 3B), and TG (FIG. 3C). Diamonds, 17ΔPst (500 PFU); squares, 17ΔPstR (500 PFU); triangles, 17ΔPst (50,000 PFU); X's, 17ΔPstR (50,000 PFU).

FIG. 4 shows HSV-1 DNA detected in the TG of rabbits 30 days after infection with high and low doses of LAT^+ and LAT^- viruses. Total TG DNA was isolated from rabbits infected with 50,000 or 500 PFU of either 17ΔPst or 17ΔPstR, and HSV-1 DNA was detected by PCR™ analysis. HSV-1 DNA was detected using primers specific for the HSV-1 DNA polymerase gene, and primers specific for the rabbit β-actin gene were used as an internal control. A titration mixture of dilutions of a cloned target plasmid containing the HSV-1 DNA polymerase target sequences was spiked into DNA extracted from an uninfected rabbit TG to generate a standard curve.

FIG. 5 shows HSV-1 DNA detected in the TG of rabbits 14 days after infection with a nonreplicating HSV-1 recombinant. Total TG DNA was isolated from rabbits infected with 500,000 PFU of either KD6, a nonreplicating (ICP4$^-$) recombinant, or wild-type 17*syn*+. The left panels show HSV-1 DNA samples obtained using primers specific for the HSV-1 DNA polymerase gene and primers specific for the rabbit β-actin gene as an internal control. The right panels show PCR™ analysis of the same samples using primers specific for the ICP4 gene and β-actin as the internal control. The dash indicates the location of the ICP4-specific product. L, left TG; R, right TG.

FIG. 6A and **FIG 6B** show an expanded view of a portion of the HSV-1 UL, internal RL and RS, US and terminal RS regions illustrating the location of tandem CTCF motifs (FIG. 6A). FIG. 6B shows a linear diagram of a portion of the genome labeled with relative locations of CTCF clusters and immediate-early genes. The sequences of the motifs are shown in Table 10.

FIG. 7A, FIG. 7B and **FIG. 7C** show ChIP analysis of identified CTCF motif clusters within latent HSV-1 DNA using antiserum specific for anti-CTCF. DRG from mice latently infected with HSV-1 strain 17*syn*+ were processed and subjected to ChIP analysis as described. The relative enrichment of CTCF at respective motif clusters was determined by PCR™ analysis of the ChIP fraction (Lane 6-8) relative to dilutions of the input material (Lane 1-4). Lane 5 is the no-input control. In FIG. 7A, ChIPs were validated using results published by Chao *et al.* (2002) by performing PCRs on titrated input and 1/10 dilution of bound ChIP sample with primers to cellular target *Tsix* imprinting/choice center CTCF-site A (positive control) and MT498 (negative control). FIG. 7B shows PCRs performed with the same titrated input and bound ChIP sample with primers to the CT1, CT4/5, and gC viral targets. FIG. 7C shows PCRs performed with titrated input and 1/100 dilution of bound ChIP sample with primers to the CT2 and gC viral targets. Band intensities of PCR™ products generated with ChIP-precipitated DNA were quantitated with respect to two-fold dilutions of input and used to demonstrate fold enrichments.

FIG. 8A and FIG. 8B show clustered CTCF binding sites are conserved across the Alphaherpesvirus family and bound the immediate-early genes. Sequence analysis was performed using a tandem repeats finder program to analyze DNA sequences (Benson, 1999). Analyses include HSV-1 strain 17syn+, HSV-2 strain HG52, Cercopithecine herpesvirus 1 (monkey B virus), Suid herpesvirus 1 (pseudorabies virus), and Human herpesvirus 3 strain Dumas (varicella-zoster virus). Solid black triangles represent consensus CCCTC or CTCCC clusters. Open white triangles represent nonconsensus CCCGC, CGCCC, CCCTG, or GTCCC clusters. Partial solid/open triangles represent clusters composed of interleaved consensus and non-consensus motifs. The pointed end of each triangle reflects the DNA strand direction (direct or complement).

FIG. 9A and FIG. 9B. FIG. 9A. Diagram of the expression cassettes of 4 transient assay plasmids that were constructed to evaluate the enhancer-blocking activity of the HSV-1 B2 insulator. All constructs employed the luciferase gene as the reporter, and the SV40 promoter. The first construct

was used to test the basal level of transcription of the SV40 promoter. The second construct contains the LAT enhancer (LTE) to assess the level of enhancement of the SV40 promoter by the LTE. The third construct contains the B2 insulator to assess any effect of the insulator region alone on SV40 promoter activity, and finally the forth construct places the B2 insulator between the enhancer and the SV40 promoter to assay for enhancer-blocking activity. **FIG. 9B.** Results of the enhancer-blocking assay. The constructs were each transfected (along with a second plasmid containing a renilla luciferase expression cassette to control for transfection efficiency) into rabbit skin cells. The results show the normalized luciferase activity (relative to the SV40 promoter-alone construct) and indicate that B2 insulator is capable of strongly blocking the activity of the LAT enhancer.

FIG. 10A and FIG. 10B. Schematic Diagram of Additional Insulator Elements within the HSV-1 Genome. **FIG. 10A.** Linear depiction of the location of the insulators in the R_L, R_S and U_S regions of the HSV-1 genome. Locations of the insulators are indicated by the triangles. Insulators B1 and B2 are shown larger (and in bold). Additional insulators are numbered B3 – B8. **FIG. 10B.** Circular depiction of the genome (as exists naturally during latency) shows the potential of the additional insulators to partition the genome into separate, independently regulated chromatin domains.

FIG. 11A and FIG. 11B. Clustered CTCF binding sites are conserved across the Alphaherpesvirus family and flank the immediate-early genes. **FIG. 11A.** An algorithm was used to analyze the HSV-1 strain 17*syn*+ genome and each respective genome in 1000-bp segments to determine the frequency with which CTCF binding sites (and potential insulators) occur in the positive (direct) or negative (complement) DNA strands. Additionally, tandem repeat analysis was performed to characterize the CTCF motif clustering (1). Analyses were performed using published NCBI GenBank sequence for HSV-2 strain HG52 (NC_001798; McGeoch, D.J.), Suid herpesvirus 1 (pseudorabies virus) (BK001744 ; Enquist, L.W.), Human herpesvirus 3 strain Dumas (varicella-zoster virus) (X04370 ; Scott, J.E.), and Cercopithecine herpesvirus 1 (monkey B virus) (NC_004812 ; Hilliard, J.K.). **FIG. 11B.** Representative CTCF pentanucleotide motifs found clustered within the Alphaherpesvirus family members. The solid triangles represent consensus CTCF motifs previously described to bind CTCF. The open triangles represent non-consensus CTCF pentanucleotide motifs. Partial solid/open triangles represent clusters composed of interleaved consensus and non-consensus motifs. The pointed end of each triangle reflects the DNA strand direction (direct or complement).

FIG. 12A and FIG. 12B. Plasmid-like viral vectors for gene delivery that embody the novel insulators derived from herpesvirus; titled Insulated Viral Artificial Chromosome (IVAC). **FIG. 12A.** pIVAC_1.0 vector contains the disclosed novel insulators surrounding neuronal-specific Latency-Associated Promoter 1 (LAP1) promoter and Long Term Expression (LTE) enhancer components, LacZ reporter gene, SV40 PolyA signal for transcription termination, insulator B4 which may contain sequence required for herpesvirus packaging into virion particles, ampicillin resistance gene for selection of the vector within bacterial cells, and the ColE1 origin of replication for high-copy number

replication of the vector within E. *coli*. **FIG. 12B.** pIVAC_1.1 vector represents an extension of pIVAC_1.0 by including all identified insulator sequences from HSV-1 to form a compound insulated vector where several genes may be inserted between insulators and individually regulated within the context of one IVAC vector.

4.0 DESCRIPTION OF ILLUSTRATIVE EMBODIMENTS

Illustrative embodiments of the invention are described below. In the interest of clarity, not all features of an actual implementation are described in this specification. It will of course be appreciated that in the development of any such actual embodiment, numerous implementation-specific decisions must be made to achieve the developers' specific goals, such as compliance with system-related and business-related constraints, which will vary from one implementation to another. Moreover, it will be appreciated that such a development effort might be complex and time-consuming, but would nevertheless be a routine undertaking for those of ordinary skill in the art having the benefit of this disclosure.

The present invention provides genetic compositions and methods to facilitate sustained administration of one or more therapeutic agents in a regulatable fashion to selected cells and tissues within a mammal, including for example, the human central nervous system. These compositions also prolong general mammalian gene expression, and provide methods for generating animal models of human disease.

The present invention relates to a eukaryotic/mammalian gene expression cassette. Due to novel insulator/boundary elements, the expression cassette can be used for directing permanent regulatable expression of heterologous genes in eukaryotic cells. As such it could be applied to viral vectors for gene delivery, direct gene therapy, transgenic animals, and the development of animal disease models.

Key elements of this invention are derived from Herpes Simplex Virus Type 1 (HSV-1). Herpesviruses possess a unique neurotropic lifestyle characterized by their ability to remain latent in neurons for the lifetime of the infected host cell. The herpes simplex virus type I is an example of the Alphaherpesvirus subfamily that has evolved a unique lifestyle that permits lytic infection in some cell types and the establishment of latency within neurons. Throughout latency, the circularized genome is maintained as a stable nucleosomal episome. Unlike lytic phase transcription, the latent phase transcriptional profile is characterized by the expression of one transcript, the latency-associated transcript (LAT), while the remainder of the genome remains largely transcriptionally silent.

The LAT locus maps to two inverted long repeat units that compose <12% of the total genome. Although this represents an overall small investment in genetic information, it is clear that the LAT locus represents an evolutionarily crucial adaptation required for the viral life-cycle. Aside from LAT, several key immediate-early genes that promote lytic phase transcription also map within this region,

although they remain transcriptionally repressed during latency. This extraordinary ability of the LAT locus to escape transcriptional repression suggested that this locus was transcriptionally-privileged and insulated from the repressive effects of the surrounding genome despite its proximity to repressed lytic-phase genes. It has been recently demonstrated that the basis of this region's ability to escape transcriptional repression is at the level of chromatin structure. This unique characteristic further suggested that with suitable development, components of this region may be exploited in the construction of expression cassette(s) that are capable of facilitating persistent/permanent regulatable gene expression. With modification, these novel insulator/boundary elements provide a useful tool for the development of transgenic animals devoid of PEV in addition to the development of constructs for gene therapy, vaccine production, and methods of assaying for gene function.

4.1 EPIGENETIC REGULATION OF HSV-1 LATENT GENE EXPRESSION

HSV-1 latency in sensory neurons is characterized by abundant expression from only one region of the genome: that encoding the HSV-1 latency associated transcript (LAT). The mechanism by which lytic gene expression is repressed is unknown, but the fact that when cellular promoters are placed in the context of the HSV-1 genome are also rapidly silenced as the virus goes latent suggests a global and epigenetic mechanism is involved. It has been previously demonstrated that H3 histones associated with HSV-1 lytic gene promoters are *hypo*acetylated, whereas ones associated with the LAT promoter/enhancer region are *hyper*acetylated during latency. This demonstrates the HSV-1 genome is ordered into different chromatin domains and suggests that insulator elements, such as those that organize cellular chromatin exist the HSV-1 genome to act as boundaries separating transcriptionally non-permissive chromatin from active chromatin domains. In support of this hypothesis, several clusters of tandemly repeated binding motifs have been identified for the cellular insulator protein CTCF, and their placement in the HSV-1 genome is consistent with chromatin boundary locations. CTCF-containing insulators have been shown to act as boundary elements, enhancer-blockers as well as silencers. Data have shown that at least one of these elements (which has been termed B2) that separate the LAT enhancer from the ICP0 region possesses enhancer-blocking activity.

4.2 HSV-1 LATENCY

Herpes simplex virus type 1 (HSV-1) typically initiates infection of the host on epithelial surfaces of the face where the virus replicates locally and spreads to the sensory ganglia of the peripheral nervous system, such as the trigeminal ganglion (TG). While the virus replicates productively in some neurons of the sensory ganglia, in others it establishes a lifelong-latent infection. Periodically, in response to various forms of physiological stress, the virus reactivates and spreads back to the epithelial surface near the site of the original infection, using the nerve axons for transport.

While reactivation may occur relatively frequently, it is usually sub-clinical, and only a small percent of the total latent population reactivates at any one time.

4.3 HSV-1 LATENT TRANSCRIPTION

A hallmark of the HSV-1 latent infection of sensory neurons is that only one region of the viral genome is actively and abundantly transcribed, the region encoding the latency associated transcript or LAT. The LAT is an 8.3 – 8.5 kb poly A RNA that is spliced to yield a 2.0-kb and 1.5-kb intron. Because the intron does not de-branch properly, it is maintained as a stable lariat and has a half-life of over 24 hours. It is this stable intron (also referred to as the major LAT) that was first detected abundantly accumulating in the nuclei of latent neurons, and has been used as a marker for HSV-1 latency. The LAT promoter (LAP1) is transcriptionally complex, and contains elements that resemble cellular promoters more so than other viral lytic promoters. Nonetheless, it has been shown that a downstream enhancer (LTE) is required for full activity of LAP1 as well as for continued expression during latency. While the precise function of the LAT RNA is unknown, deletions of either the LAP1 or the LTE result in a reduced ability to reactivate. In addition, other LAT deletions have been shown to reduce the efficiency of establishment of latency, and be involved in neuronal protection and apoptosis.

While LAT is abundantly transcribed during latency, HSV-1 lytic gene expression is repressed. The basis for this repression is unknown. It has been proposed that the lack of activation of the HSV-1 immediate early genes IE genes is due to the fact that certain neurons possess low levels of the cellular transcription factor Oct 1, and this low level of abundance is responsible for the failure to initiate the lytic cascade. However, this doesn't explain how leaky IE gene activity would be repressed, or more importantly why heterologous cellular promoters that are placed in the context of the HSV-1 genome are rapidly silenced. Instead, these observations suggest that a more global and dynamic mechanism is involved in silencing HSV-1 lytic genes during latency. The gradual and global nature of the silencing of HSV-1 lytic genes and transgenes suggested that an epigenetic mechanism such as DNA methylation or histone modifications might play a role in suppressing transcription. Analyses of latent HSV-1 genomes have demonstrated that specific histone modifications (and not DNA methylation) correlate with transcriptional activity of the viral genome during latency. This suggests that histone modifications may play a similar role in regulating HSV-1 latent transcription epigenetically, as they do in regulating transcriptional activity of cellular chromatin.

4.4 SPECIFIC HISTONE MODIFICATIONS CORRELATE WITH TRANSCRIPTIONAL PERMISSIVENESS

Patterns of specific histone modifications have been shown to act as epigenetic markers of eukaryotic gene expression. Specific combinations of acetylation, methylation, phosphorylation and

ubiquitination of residues of the N-terminal tails of histones, especially H3 and H4, are associated with differences in transcriptional permissivity has been termed the "histone code". For example, transcriptionally active euchromatin is typically rich in histone H3 acetylated at lysines 9 and 14 (acetyl H3 K9, K14), whereas transcriptionally repressed heterochromatin is typically enriched in histone H3 methylated at the lysine 9 position (H3 K9 trimethyl). These epigenetic markers not only act as markers of the "transcriptional history" of a particular segment of chromatin, but in many cases also recruit cellular enzymes such as Pol II or other chromatin modifying enzymes.

The study of which specific histones are associated with a particular gene or promoter has been greatly facilitated by the availability of specific antisera against individual histone modifications. These antisera are used in chromatin immunoprecipitation assays (ChIP) where the histones are cross-linked to the DNA with formaldehyde, the DNA sonicated into 500 – 1000 bp fragments, followed by immunoprecipitation with the specific antiserum. The regions of DNA that are associated with the particular histone are identified by PCR, where the precipitated (enriched) chromatin is compared with the input or unbound fraction. By using PCR primers to compare different regions of a chromosome, one can generate a profile of the changes in transcriptional permissiveness as a function of specific histones that are bound.

4.5 CELLULAR CHROMOSOMES ARE ORGANIZED INTO CHROMATIN DOMAINS: REGIONS OF DIFFERING TRANSCRIPTIONAL PERMISSIVENESS

It has long been known that certain regions of cellular chromosomes tended to contain transcriptionally active genes, whereas others (such as the centromeres) were transcriptionally silent. ChIP analyses have expanded this view to provide a higher resolution picture of genes clusters that are transcriptionally permissive. As might be expected, the histone composition of clusters of housekeeping genes is similar amongst different cell and tissue types. On the other hand, developmentally regulated genes and genes that confer cell-specific functions are often clustered, and these cell-type specific transcription domains often possess dramatically different histone profiles. These observations have led to the development of models whereby chromatin is organized into domains based largely on function and transcriptional activity. The identification of regulatory regions flanking many of these domains has shown these regions specifically recruit histone-modifying enzymes that permit the establishment and maintenance of transcriptionally active or transcriptionally repressive histone modifications. Insulators are a class of these *cis*-acting factors that have been shown to regulate the establishment of chromatin domains.

4.6 ROLE OF INSULATORS BOUNDARIES, ENHANCERS AND SILENCERS IN MAINTAINING THE INTEGRITY OF TRANSCRIPTIONAL DOMAINS

Chromatin domains are regions of chromatin with similar transcriptional permissivity and that contain similar types of modified histones. **Insulators** are a general class of *cis*-acting elements at the boundary of a transcriptional domain that partition the domain from surrounding chromatin regions. Transcriptionally active chromatin domains often contain an **enhancer** that promotes a transcriptionally active state within that chromatin domain. In contrast, a transcriptionally silent chromatin domain may contain a **silencer** element, which promotes the formation of transcriptionally repressive heterchromatin within that domain. Insulator elements that flank transcriptionally distinct chromatin domains must effectively insulate one domain from the effects of the enhancer or silencer located in the other.

There are actually several different sub-types of chromatin insulators that are defined based on differences in their functional properties. A boundary or **barrier** insulator is one that acts to separate one distinct region of chromatin from another. For example a boundary might separate a region of heterochromatin enriched in H3 K9 Me, from a region enriched in H3 (K9, K14) Ac. An insulator can also have **enhancer-blocking** activity, and prevent enhancing activity from acting upstream of the insulator. In an analogous manner, insulators with **barrier** activity can block the effect of a silencer, and prevent the spread of heterochromatin from going beyond the barrier element. An important point is that typically, enhancer-blocking and barrier activities of an insulator are polar, and only work in one direction. In addition, an enhancer blocker is specific for blocking the effects of an enhancer, but may not necessarily block the effects of a silencer. Clearly it has been shown that insulator elements act not only to segregate regions of differing chromatin composition, but have also been shown to play a dynamic role in the formation of the chromatin environment on either side of the boundary. This process is mediated by the recruitment of chromatin modifying enzymes, such as histone methyltransferases, histone deacetylases, and histone acetylatransferases. Insulator regions of the genome therefore can be thought of as nucleation sites for the formation of multi-protein complexes that confer different activities and functions based upon their protein composition.

4.7 ROLE OF THE CELLULAR INSULATOR PROTEIN CTCF IN FORMING CHROMATIN BOUNDARIES

All known vertebrate insulators that have been characterized to date bind "CCCTC-binding factor" or CTCF. CTCF is an eleven-zinc finger-containing DNA-binding protein that is highly conserved among vertebrates. CTCF is ubiquitously expressed in most cell types and possesses transcriptional activator activity that is regulated by phosphorylation. In addition to "CCCTC", it also binds to several other pentanucleotide motifs. While a single DNA binding motif has been shown to be sufficient for binding, the binding motifs are often present as clusters of these consensus sequences and

the binding to multiple CTCF motif sites affords higher binding affinity. While CTCF binding results in a number of distinct activities, including gene activation and repression, its function in the formation and regulation of chromatin insulators is mediated through interactions with other chromatin-modifying proteins. CTCF has also been proposed to be an essential scaffolding component of chromatin boundaries that may help promote the formations of chromatin loops that attach to specific regions of the nuclear lamina and that segregate chromatin into spatially-separated chromatin domains.

4.8 THE LAT PROMOTER (LAP1) IS THE ONLY HSV-1 PROMOTER ACTIVE DURING LATENCY

The LAT promoter (LAP1) has been shown to be able to drive the expression of a heterologous transgene in mouse sensory ganglia neurons after lytic gene expression had subsided. The LAP1 is arguably one of the most transcriptionally-complex promoters in the HSV-1 genome and contains a number of binding sites for cellular transcription factors including CRE, USF and SP1. Deletion of the core LAP1 promoter elements (202-bp *Pst*I fragment) results in abolishing all detectable LAT expression by *in situ* hybridization, and >1000-fold reduction in detectable RNA by RT-PCR analysis. In addition, several regions have been that contain elements essential for neuron-specific expression. An additional promoter (LAP2) located downstream of LAP1 has been shown to have some activity during the lytic phase of infection, but not during the latent infection.

While the LAP1 promoter is active during latency, lytic gene promoters fail to drive detectable transgene expression during latency, and lytic gene RNA is below the level of detection in many studies employing Northern blot or RT-PCR analyses. While assessment of RNA levels using very sensitive RT-PCR of latently infected ganglia has detected very low amounts of some viral genes such as tk and ICP4, a recent study argued that these RNAs are likely due to an occasional "spontaneous" reactivating neuron, an event that apparently occurs more frequently than was originally thought. These studies have demonstrated that the LAT is the only abundantly transcribed RNA during HSV-1 latency, and that LAP1 directs its expression in a neuron-specific manner.

4.9 PROMOTERS OF HSV-1 LYTIC GENES ARE RAPIDLY SILENCED AS THE VIRUS ENTERS LATENCY

Numerous studies have demonstrated that HSV-1 lytic genes are silenced as the virus enters latency. Following infection of mice by the footpad (f.p.) route, the virus replicates locally in the epithelium to the foot, and then spreads to the dorsal root ganglia (DRG), where acute replication peaks at day 4 (at an inoculum of 5×10^3 pfu/mouse). By 14 days p.i., infectious virus and lytic gene expression are below the normal limits of detection (<1000 copies of RNA per mouse), whereas LAT RNA is abundant (>100,000 copies per mouse). Viral recombinants containing *lacZ* as a reporter have also demonstrated that lytic gene promoters such as dUTPase fail to drive detectable reporter gene

expression after day 10. Most importantly, it was shown that cellular promoters such as the mouse phosphoglycerate kinase (PGK) promoter and the metallothionine promoter are rapidly silenced as the virus enters latency. The fact that these cellular promoters contain binding sites for cellular transcription factors, and that they are functional in the context of transgenic mice (as well as from the HSV-1 genome during a lytic infection) suggests that there is a global silencing of viral lytic gene regions that occurs as the virus enters latency.

4.10 THE REPRESSION OF LYTIC GENES DURING LATENCY IS ASSOCIATED WITH SPECIFIC HISTONE MODIFICATIONS AND NOT WITH DNA METHYLATION

During HSV-1 latency, gene expression is tightly repressed except for the latency-associated transcript (LAT). The mechanistic basis for this repression is unclear, but its global nature suggests regulation by an epigenetic mechanism such as DNA methylation. Previous work demonstrated that latent HSV-1 genomes are not extensively methylated but these studies lacked the resolution to examine methylation of individual CpGs that could repress transcription from individual promoters during latency. To address this point, established models were employed to predict genomic regions with the highest probability of being methylated and using bisulfite sequencing analyzed the methylation profiles of these regions. No significant methylation of latent DNA isolated from mouse dorsal root ganglia was observed in any of the regions examined, including the ICP4 and LAT promoters. This analysis indicates methylation is unlikely to play a major role in regulating HSV-1 latent gene expression.

Chromatin immunoprecipitation (ChIP) analysis of latently infected mouse DRG involves cross-linking of the histones to the total cellular DNA, followed by sonication to randomly shear the DNA into 500 –1000 bp fragments. These fragments are then precipitated with antisera specific for a particular histone modification (such as acetyl H3 K9, K14) and the bound *vs.* unbound fractions are analyzed by PCR directed at specific regions of the viral genome to assess for relative levels of that histone that are associated with each region. ChIP of the latent HSV-1 DNA repeat regions demonstrated a portion of the LAT region is associated with histone H3 acetylated at lysine 9 and 14, consistent with a euchromatic and non-repressed structure. In contrast, the chromatin associated with the HSV-1 DNA polymerase gene located in the unique long segment was not enriched in H3 acetylated at lysine 9 and 14 suggesting a transcriptionally inactive structure. These data suggest histone composition may be a major regulatory determinant of HSV latent gene expression.

Studies directed at establishing stable, long-term transgene expression in the context of the HSV-1 latent genome revealed that the LAT promoter (LAP1), by itself, was not sufficient to maintain long-term expression in peripheral ganglia. While LAP1 resulted in expression of a longer duration than other heterologous promoters examined, expression persisted only for 3-4 weeks before being silenced. It has been demonstrated that expression could be extended by the inclusion of a region

encompassing the 5' exon of LAT that acted as an enhancer for LAT promoter activity as well. This LAT enhancer (LTE) was demonstrated to act in both upstream and downstream positions. These data demonstrated that the LTE acts not only as an enhancer of the LAT promoter, but also acts to maintain long-term expression from this promoter during latency.

4.11 FUNCTIONAL ACTIVITY OF THE HSV-1 B2 INSULATOR ELEMENT

One of the functional characteristics of the insulator elements is the ability to isolate gene expression cassettes from the repressive effects of chromatin surrounding where the insulator cassette is inserted. To this end, several transient assay plasmids have been generated that have permitted the demonstration that the insulator element **B2** has enhancer-blocking activity.

4.12 CHARACTERIZATION OF HSV INSULATOR ELEMENTS

The HSV-1 insulator elements (depicted in FIG. 1 and FIG. 2) and now referred to as **B1** and **B2** are novel *cis*-acting elements capable of insulating the expression cassette and maintaining long-term sustained expression. These elements likely contain multiple binding sites for cellular factors that, in specific combination, confer this unique insulation property as well as their ability to function in a cell-type-specific manner. In order to characterize the component proteins that bind, the inventors have begun dissecting these elements. Reiterated motifs have been identified (referred to as CT-elements) that are contained in B1 and B2, and that contain reiterated binding sites for a cellular insulator protein CTCF. By chromatin immunoprecipitation assay it has been demonstrated that this protein binds to these elements on the latent HSV-1 genome. From these studies, CTCF appears to be an essential scaffolding protein for the B1 and B2 elements, however in itself, binding of this protein is insufficient to exert the key functional properties displayed by the B1 and B2 insulators. The enabling functional properties are likely contained in the regions surrounding the CT elements (FIG. 1 and FIG. 2). Yeast-one and yeast-two hybrid analyses have been employed to identify any other proteins which may be responsible for the activity of the elements. Based on initial analyses, the HSV-1 insulators appear to possess biologically-unique properties from cellular insulator elements that bind CTCF, and these properties are inherent in the unique sequence and combination of other proteins that bind to the HSV-1 insulator elements.

4.13 THE HSV-1 GENOME CONTAINS SEVERAL OTHER POTENTIAL INSULATOR ELEMENTS

Using the CT elements as a basis, 5 other unique CT element clusters have been identified in the HSV-1 genome (FIG. 10). Based on their ability to bind CTCF, these other clusters of CT elements (B3-B7) appear to have the potential to act as a type of insulator, however they likely display different functional properties from B1 and B2. For example, in their native form they may not be able to

insulate gene expression in a manner analogous to B1 and B2, however they may be modified to do so, or to display altered expression profiles for the expression cassette.

4.14 Other Herpesviruses Genomes also Contain B1 and B2 Homologs

Analyses have been performed on a number of other alphaherpesviruses (for which complete genomic sequence is available, and from these studies, similar clusters of CT elements have been identified which may also act as insulators analogous to those in HSV-1 (FIG. 11). It is likely that these elements (particularly those homologous to B1 and B2) may also be used as components of insulator cassettes. In addition, it is possible that these other herpesvirus elements could be used in conjunction with or in place of the B1 and B2 elements as they may naturally possess modified tropism properties that might be ideally suited to facilitate expression in certain cell or animal host types. Indeed the inventors contemplate that insulator elements may be identified and isolated among many different members of the Herpesvirus family. In addition to the alphaherpesviruses, betaherpesviruses and gammaherpesviruses may also represent important sources for obtaining the insulator elements disclosed in the present invention.

4.15 Uses of HSV-1 Insulator Cassettes in Gutted HSV Vectors

FIG. 12A and FIG. 12B show schematics for a specific example of the use of the HSV-1 insulator cassette in the context of an HSV-1 vector. This is a "gutted" HSV-1 vector, deleted in HSV-1 essential genes (similar to an amplicon). A novel feature of the vector shown in FIG. 12A is that this vector (now termed Insulated Viral Artificial Chromosome or *IVAC*) contains insulators B1 and B2 bounding the expression cassette thereby enabling sustained long-term expression. This herpes-based example is just one possible implementation of the technology in the context of viral (IVAC) vectors.

4.16 Gene Therapy Vectors

The field of gene therapy offers a promising therapeutic strategy for the treatment of a wide variety of human diseases of the central nervous system including Alzheimer's, Parkinson's, Huntington's Diseases and Fragile-X Mental Retardation Syndrome as examples. Many chronic and progressive diseases require sustained or regulatable administration of the therapeutic gene to achieve successful treatment. Unfortunately, progress *via* conventional gene therapy has been slow as a result of transgene down-regulation due to host cell silencing mechanisms. These mechanisms include, but are not limited to, histone methylation/deacetylation, DNA methylation, position effects, or transgene copy number. This has limited the usefulness of current gene therapy vector technology for developing treatments for chronic and progressive genetic disorders. This invention addresses this problem by providing a novel set of control elements that permit a gene expression cassette to be insulated from the effects of surrounding DNA, and possesses structural features that maintain a transcriptionally

accessible and regulatable environment for the expression of transgenes in a number of viral and cellular systems.

In illustrative embodiments, Herpes Simplex Virus type 1 vectors may be utilized to deliver the gene expression cassettes, because they have many advantages when considering gene delivery vectors. These include the ability to package large DNA insertions. In addition, HSV-I is neurotropic and establishes life-long infection in neurons in which the genome is maintained as a stable episome. Moreover, HSV-1 maintains the ability to infect and replicate within a wide range of human cell lines with high efficiencies.

4.17 PRODUCTION OF TRANSGENIC ANIMALS

Animal models of human disease are often an invaluable asset for use in biomedical research. However, generating transgenic or knock-out animals to accurately model human disease is no trivial task. The insulated nature of the gene expression cassette provides a way to circumvent problems, such as embryonic lethals, associated with generating these animals. For example, current methods may use *cre-lox* systems to get past embryonic lethal animals, but the gene will be knocked out in all cells. Perhaps there are alternative uses for a particular gene product in various cells. The gene expression cassettes provided by the present invention represent a new and reliable method for gene knock-out within the subset of cells corresponding directly to the cell-type specific boundary and insulation effects of the cassette. Regardless, the ability to maintain the expression cassette in an accessible and transcriptionally-responsive conformation provides the opportunity to regulate gene expression at desired times in development. In addition, the genetic expression elements of the present invention may also be applied to the production of transgenic animals that are to be used for the production of large amounts of a transgene for pharmacologic or agricultural purposes.

It is contemplated that in some instances the genome of a transgenic non-human animal of the present invention will have been altered through the stable introduction of one or more of the genetic expression elements described herein, either native, synthetically modified, or mutated. In particular, such genetic expression elements may be provided to cells of such animals using viral vectors, such as, for example, HSV, lentiviral, retroviral, AV, or rAAV vectors. As used herein, the term "transgenic animal" is intended to refer to an animal that has incorporated exogenous DNA sequences into its genome. In designing a heterologous gene for expression in animals, sequences which interfere with the efficacy of gene expression, such as polyadenylation signals, polymerase II termination sequences, hairpins, consensus splice sites and the like are eliminated. Current advances in transgenic approaches and techniques have permitted the manipulation of a variety of animal genomes *via* gene addition, gene deletion, or gene modifications (Franz *et al.*, 1997). For example, mosquitoes (Fallon, 1996), trout (Ono *et al.*, 1997), zebrafish (Caldovic and Hackett, 1995), pigs (Van Cott *et al.*, 1997) and cows (Haskell and Bowen, 1995), are just a few of the many animals being studied by transgenics. The

creation of transgenic animals that express human proteins such as α-1-antitrypsin, in sheep (Carver *et al.*, 1993); decay accelerating factor, in pigs (Cozzi *et al.*, 1997), and plasminogen activator, in goats (Ebert *et al.*, 1991) has previously been demonstrated. The transgenic synthesis of human hemoglobin (U. S. Patent 5,602,306) and fibrinogen (U. S. Patent 5,639,940) in non-human animals have also been disclosed, each specifically incorporated herein by reference in its entirety. Further, transgenic mice and rat models have recently been described as new directions to study and treat cardiovascular diseases such as hypertension in humans (Franz *et al.*, 1997; Pinto-Siestma and Paul, 1997). The construction of a transgenic mouse model has recently been used to assay potential treatments for Alzheimer's disease (U. S. Patent 5,720,936, specifically incorporated herein by reference in its entirety). It is contemplated in the present invention that transgenic animals contribute valuable information as models for studying the effects of viral vector-delivered therapeutic compositions on correcting genetic defects and treating a variety of disorders in an animal.

4.18 ADENO-ASSOCIATED VIRUS

Adeno-associated virus is a single-stranded DNA-containing, non-pathogenic human parvovirus that is being widely investigated as a therapeutic vector for a host of muscle disorders (Muzyczka, 1992; Kessler *et al.*, 1996; Clark *et al.*, 1997; Fisher *et al.*, 1997). Six serotypes of the virus (AAV1-6) were originally described, and two more have recently been identified in rhesus macaques (Gao *et al.*, 2002). Recombinant adeno-associated virus (rAAV) vectors have been developed in which the *rep* and *cap* open reading frames of the wild-type virus have been completely replaced by a therapeutic or reporter gene, retaining only the characteristic inverted terminal repeats (ITRs), the sole *cis*-acting elements required for virus packaging. Using helper plasmids expressing various combinations of the AAV2 *rep* and AAV1, 2, and 5 *cap* genes, respectively, efficient cross-packaging of AAV2 genomes into particles containing the AAV1, 2, or 5 capsid protein has been demonstrated (Grimm *et al.*, 2003; Xiao *et al.*, 1999; Zolotukhin *et al.*, 2002; Rabinowitz *et al.*, 2002). The various serotype vectors have demonstrated distinct tropisms for different tissue types *in vivo*, due in part to their putative cell surface receptors. Although several reports have indicated that rAAV1 vectors efficiently transduce skeletal muscle in general (Fraites *et al.*, 2002; Chao *et al.*, 2001; Hauck and Xiao, 2003), no study to date has reported which of the serotypes, if any, might transduce the diaphragm in particular.

4.19 PROMOTERS AND ENHANCERS

Recombinant vectors form important aspects of the present invention. The term "expression vector or construct" means any type of genetic construct containing a nucleic acid in which part or all of the nucleic acid encoding sequence is capable of being transcribed. In preferred embodiments, expression only includes transcription of the nucleic acid, for example, to generate a therapeutic agent

from a transcribed gene that is comprised within one or more of the insulated HSV-derived gene expression cassettes disclosed herein.

Particularly useful vectors are contemplated to be those vectors in which the nucleic acid segment to be transcribed is positioned under the transcriptional control of a promoter. A "promoter" refers to a DNA sequence recognized by the synthetic machinery of the cell, or introduced synthetic machinery, required to initiate the specific transcription of a gene. The phrases "operatively linked," "operably linked," "operatively positioned," "under the control of" or "under the transcriptional control of" means that the promoter is in the correct location and orientation in relation to the nucleic acid segment that comprises the therapeutic gene to properly facilitate, control, or regulate RNA polymerase initiation and expression of the therapeutic gene to produce the therapeutic peptide, polypeptide, ribozyme, or antisense RNA molecule in the cells that comprise and express the genetic construct.

In preferred embodiments, it is contemplated that certain advantages will be gained by positioning the therapeutic agent-encoding polynucleotide segment under the control of one or more recombinant, or heterologous, promoter(s). As used herein, a recombinant or heterologous promoter is intended to refer to a promoter that is not normally associated with the particular therapeutic gene of interest in its natural environment. Such promoters may include promoters normally associated with other genes, and/or promoters isolated from any other bacterial, viral, eukaryotic, or mammalian cell.

Naturally, it will be important to employ a promoter that effectively directs the expression of the therapeutic agent-encoding nucleic acid segment in the cell type, organism, or even animal, chosen for expression. The use of promoter and cell type combinations for protein expression is generally known to those of skill in the art of molecular biology, for example, see Sambrook *et al.* (1989), incorporated herein by reference. The promoters employed may be constitutive, or inducible, and can be used under the appropriate conditions to direct high-level expression of the introduced DNA segment.

At least one module in a promoter functions to position the start site for RNA synthesis. The best-known example of this is the TATA box, but in some promoters lacking a TATA box, such as the promoter for the mammalian terminal deoxynucleotidyl transferase gene and the promoter for the SV40 late genes, a discrete element overlying the start site itself helps to fix the place of initiation.

Additional promoter elements regulate the frequency of transcriptional initiation. Typically, these are located in the region 30-110 bp upstream of the start site, although a number of promoters have been shown to contain functional elements downstream of the start site as well. The spacing between promoter elements frequently is flexible, so that promoter function is preserved when elements are inverted or moved relative to one another. In the tk promoter, the spacing between promoter elements can be increased to 50 bp apart before activity begins to decline. Depending on the promoter, it appears that individual elements can function either co-operatively or independently to activate transcription.

The particular promoter that is employed to control the expression of a nucleic acid is not believed to be critical, so long as it is capable of expressing the nucleic acid in the targeted cell. Thus, where a human cell is targeted, it is preferable to position the nucleic acid coding region adjacent to and under the control of a promoter that is capable of being expressed in a human cell. Generally speaking, such a promoter might include either a human or viral promoter, such as a β-actin, AAV, AV, CMV or HSV promoter. In certain aspects of the invention, inducible promoters, such as tetracycline-controlled promoters, are also contemplated to be useful in certain cell types.

In various other embodiments, the human cytomegalovirus (CMV) immediate early gene promoter, the SV40 early promoter and the Rous sarcoma virus long terminal repeat can be used to obtain high-level expression of transgenes. The use of other viral or mammalian cellular or bacterial phage promoters that are well known in the art to achieve expression of a transgene is contemplated as well, provided that the levels of expression are sufficient for a given purpose. Tables 1 and 2 below list several elements/promoters that may be employed, in the context of the present invention, to regulate the expression of the therapeutic agents that are comprised within the disclosed insulated HSV-derived gene expression constructs. This list is not intended to be exhaustive of all the possible elements involved in the promotion of transgene expression but, merely, to be exemplary thereof.

Enhancers were originally detected as genetic elements that increased transcription from a promoter located at a distant position on the same molecule of DNA. This ability to act over a large distance had little precedent in classic studies of prokaryotic transcriptional regulation. Subsequent work showed that regions of DNA with enhancer activity are organized much like promoters. That is, they are composed of many individual elements, each of which binds to one or more transcriptional proteins.

The basic distinction between enhancers and promoters is operational. An enhancer region as a whole must be able to stimulate transcription at a distance; this need not be true of a promoter region or its component elements. On the other hand, a promoter must have one or more elements that direct initiation of RNA synthesis at a particular site and in a particular orientation, whereas enhancers lack these specificities. Promoters and enhancers are often overlapping and contiguous, often seeming to have a very similar modular organization.

Additionally any promoter/enhancer combination (as per the Eukaryotic Promoter Data Base EPDB) could also be used to drive expression. Use of a T3, T7 or SP6 cytoplasmic expression system is another possible embodiment. Eukaryotic cells can support cytoplasmic transcription from certain bacterial promoters if the appropriate bacterial polymerase is provided, either as part of the delivery complex or as an additional genetic expression construct.

TABLE 1
PROMOTER AND ENHANCER ELEMENTS

PROMOTER/ENHANCER	REFERENCES
Immunoglobulin Heavy Chain	Banerji *et al.*, 1983; Gilles *et al.*, 1983; Grosschedl and Baltimore, 1985; Atchinson and Perry, 1986, 1987; Imler *et al.*, 1987; Weinberger *et al.*, 1984; Kiledjian *et al.*, 1988; Porton *et al.*; 1990
Immunoglobulin Light Chain	Queen and Baltimore, 1983; Picard and Schaffner, 1984
T-Cell Receptor	Luria *et al.*, 1987; Winoto and Baltimore, 1989; Redondo *et al.*; 1990
HLA DQ a and DQ β	Sullivan and Peterlin, 1987
β-Interferon	Goodbourn *et al.*, 1986; Fujita *et al.*, 1987; Goodbourn and Maniatis, 1988
Interleukin-2	Greene *et al.*, 1989
Interleukin-2 Receptor	Greene *et al.*, 1989; Lin *et al.*, 1990
MHC Class II 5	Koch *et al.*, 1989
MHC Class II HLA-Dra	Sherman *et al.*, 1989
β-Actin	Kawamoto *et al.*, 1988; Ng *et al.*; 1989
Muscle Creatine Kinase	Jaynes *et al.*, 1988; Horlick and Benfield, 1989; Johnson *et al.*, 1989
Prealbumin (Transthyretin)	Costa *et al.*, 1988
Elastase I	Orntz *et al.*, 1987
Metallothionein	Karin *et al.*, 1987; Culotta and Hamer, 1989
Collagenase	Pinkert *et al.*, 1987; Angel *et al.*, 1987a
Albumin Gene	Pinkert *et al.*, 1987; Tronche *et al.*, 1989, 1990
α-Fetoprotein	Godbout *et al.*, 1988; Campere and Tilghman, 1989
t-Globin	Bodine and Ley, 1987; Perez-Stable and Constantini, 1990
β-Globin	Trudel and Constantini, 1987
e-fos	Cohen *et al.*, 1987
c-HA-ras	Triesman, 1986; Deschamps *et al.*, 1985
Insulin	Edlund *et al.*, 1985
Neural Cell Adhesion Molecule (NCAM)	Hirsh *et al.*, 1990
$\alpha_{1\text{-Antitrypain}}$	Latimer *et al.*, 1990
H2B (TH2B) Histone	Hwang *et al.*, 1990
Mouse or Type I Collagen	Ripe *et al.*, 1989
Glucose-Regulated Proteins (GRP94 and GRP78)	Chang *et al.*, 1989
Rat Growth Hormone	Larsen *et al.*, 1986

PROMOTER/ENHANCER	REFERENCES
Human Serum Amyloid A (SAA)	Edbrooke *et al.*, 1989
Troponin I (TN I)	Yutzey *et al.*, 1989
Platelet-Derived Growth Factor	Pech *et al.*, 1989
Duchenne Muscular Dystrophy	Klamut *et al.*, 1990
SV40	Banerji *et al.*, 1981; Moreau *et al.*, 1981; Sleigh and Lockett, 1985; Firak and Subramanian, 1986; Herr and Clarke, 1986; Imbra and Karin, 1986; Kadesch and Berg, 1986; Wang and Calame, 1986; Ondek *et al.*, 1987; Kuhl *et al.*, 1987; Schaffner *et al.*, 1988
Polyoma	Swartzendruber and Lehman, 1975; Vasseur *et al.*, 1980; Katinka *et al.*, 1980, 1981; Tyndell *et al.*, 1981; Dandolo *et al.*, 1983; de Villiers *et al.*, 1984; Hen *et al.*, 1986; Satake *et al.*, 1988; Campbell and Villarreal, 1988
Retroviruses	Kriegler and Botchan, 1982, 1983; Levinson *et al.*, 1982; Kriegler *et al.*, 1983, 1984a, b, 1988; Bosze *et al.*, 1986; Miksicek *et al.*, 1986; Celander and Haseltine, 1987; Thiesen *et al.*, 1988; Celander *et al.*, 1988; Choi *et al.*, 1988; Reisman and Rotter, 1989
Papilloma Virus	Campo *et al.*, 1983; Lusky *et al.*, 1983; Spandidos and Wilkie, 1983; Spalholz *et al.*, 1985; Lusky and Botchan, 1986; Cripe *et al.*, 1987; Gloss *et al.*, 1987; Hirochika *et al.*, 1987; Stephens and Hentschel, 1987
Hepatitis B Virus	Bulla and Siddiqui, 1986; Jameel and Siddiqui, 1986; Shaul and Ben-Levy, 1987; Spandau and Lee, 1988; Vannice and Levinson, 1988
Human Immunodeficiency Virus	Muesing *et al.*, 1987; Hauber and Cullan, 1988; Jakobovits *et al.*, 1988; Feng and Holland, 1988; Takebe *et al.*, 1988; Rosen *et al.*, 1988; Berkhout *et al.*, 1989; Laspia *et al.*, 1989; Sharp and Marciniak, 1989; Braddock *et al.*, 1989
Cytomegalovirus	Weber *et al.*, 1984; Boshart *et al.*, 1985; Foecking and Hofstetter, 1986
Gibbon Ape Leukemia Virus	Holbrook *et al.*, 1987; Quinn *et al.*, 1989

TABLE 2
INDUCIBLE ELEMENTS

ELEMENT	INDUCER	REFERENCES
MT II	Phorbol Ester (TFA) Heavy metals	Palmiter *et al.*, 1982; Haslinger and Karin, 1985; Searle *et al.*, 1985; Stuart *et al.*, 1985; Imagawa *et al.*, 1987, Karin *et al.*, 1987; Angel *et al.*, 1987b; McNeall *et al.*, 1989
MMTV (mouse mammary tumor virus)	Glucocorticoids	Huang *et al.*, 1981; Lee *et al.*, 1981; Majors and Varmus, 1983; Chandler *et al.*, 1983; Lee *et al.*, 1984; Ponta *et al.*, 1985; Sakai *et al.*, 1988

ELEMENT	INDUCER	REFERENCES
β-Interferon	poly(rI)x poly(rc)	Tavernier *et al.*, 1983
Adenovirus 5 E2	Ela	Imperiale and Nevins, 1984
Collagenase	Phorbol Ester (TPA)	Angel *et al.*, 1987a
Stromelysin	Phorbol Ester (TPA)	Angel *et al.*, 1987b
SV40	Phorbol Ester (TPA)	Angel *et al.*, 1987b
Murine MX Gene	Interferon, Newcastle Disease Virus	
GRP78 Gene	A23187	Resendez *et al.*, 1988
α-2-Macroglobulin	IL-6	Kunz *et al.*, 1989
Vimentin	Serum	Rittling *et al.*, 1989
MHC Class I Gene H-2κb	Interferon	Blanar *et al.*, 1989
HSP70	Ela, SV40 Large T Antigen	Taylor *et al.*, 1989; Taylor and Kingston, 1990a, b
Proliferin	Phorbol Ester-TPA	Mordacq and Linzer, 1989
Tumor Necrosis Factor	FMA	Hensel *et al.*, 1989
Thyroid Stimulating Hormone a Gene	Thyroid Hormone	Chatterjee *et al.*, 1989

As used herein, the terms "engineered" and "recombinant" cells are intended to refer to a cell into which an exogenous nucleic acid segment, such as DNA segment that leads to the transcription of a therapeutic agent, such as a therapeutic peptide, polypeptide, ribozyme, antisense, or catalytic mRNA molecule has been introduced. Therefore, engineered cells are distinguishable from naturally occurring cells, which do not contain a recombinantly introduced exogenous polynucleotide segment. Engineered cells are thus cells having nucleic acid segment introduced through the hand of man.

To express a therapeutic gene in accordance with the present invention one would prepare an insulated HSV-derived gene expression vector that comprises at least a first sequence region that encodes a therapeutic peptide polypeptide ribozyme or antisense mRNA under the control of one or more promoters. To bring a sequence "under the control of" a promoter, one positions the 5' end of the transcription initiation site of the transcriptional reading frame generally between about 1 and about 50 nucleotides "downstream" of (*i.e.*, 3' of) the chosen promoter. The "upstream" promoter stimulates transcription of the DNA and promotes expression of the encoded polypeptide. This is the meaning of "recombinant expression" in this context.

4.20 PHARMACEUTICAL COMPOSITIONS

In certain embodiments, the present invention concerns formulation of one or more of the insulated HSV-derived gene expression cassettes disclosed herein in pharmaceutically acceptable solutions for administration to a cell or an animal, either alone, or in combination with one or more other modalities of therapy. In particular, the present invention contemplates the formulation of one or more viral vectors, virions, or virus particles (or pluralities thereof) that comprise one or more of the disclosed insulated HSV-derived gene expression cassettes.

In such pharmaceutical compositions, it will also be understood that, if desired, the encoded nucleic acid segment, RNA, DNA or PNA compositions that express one or more therapeutic gene product(s) as disclosed herein may be administered in combination with other agents as well, such as, *e.g.*, peptides, proteins or polypeptides or various pharmaceutically-active agents, including one or more systemic or topical administrations of viral vector formulations described herein. In fact, there is virtually no limit to other components that may also be included, given that the additional agents do not cause a significant adverse effect upon contact with the target cells or host tissues. The viral vector compositions may thus be delivered along with various other agents as required in the particular instance. Such compositions may be purified from host cells or other biological sources, or alternatively may be chemically synthesized as described herein. Likewise, such compositions may further comprise substituted or derivatized RNA, DNA, or PNA compositions.

Formulation of pharmaceutically-acceptable excipients and carrier solutions is well-known to those of skill in the art, as is the development of suitable dosing and treatment regimens for using the particular compositions described herein in a variety of treatment regimens, including *e.g.*, oral, topical, sublingual, subcutaneous, transdermal, parenteral, intravenous, intranasal, and intramuscular administration and formulation.

In certain circumstances it will be desirable to deliver the pharmaceutical compositions disclosed herein parenterally, intravenously, intramuscularly, or even intraperitoneally as described in U.S. Patent 5,543,158; U.S. Patent 5,641,515 and U.S. Patent 5,399,363 (each specifically incorporated herein by reference in its entirety). Solutions of the active compounds as freebase or pharmacologically acceptable salts may be prepared in water suitably mixed with a surfactant, such as hydroxypropylcellulose. Dispersions may also be prepared in glycerol, liquid polyethylene glycols, and mixtures thereof and in oils. Under ordinary conditions of storage and use, these preparations contain a preservative to prevent the growth of microorganisms.

The pharmaceutical forms suitable for injectable use include sterile aqueous solutions or dispersions and sterile powders for the extemporaneous preparation of sterile injectable solutions or dispersions (U.S. Patent 5,466,468, specifically incorporated herein by reference in its entirety). In all cases the form must be sterile and must be fluid to the extent that easy syringability exists. It must be stable under the conditions of manufacture and storage and must be preserved against the

contaminating action of microorganisms, such as bacteria and fungi. The carrier can be a solvent or dispersion medium containing, for example, water, ethanol, polyol (*e.g.*, glycerol, propylene glycol, and liquid polyethylene glycol, and the like), suitable mixtures thereof, and/or vegetable oils. Proper fluidity may be maintained, for example, by the use of a coating, such as lecithin, by the maintenance of the required particle size in the case of dispersion and by the use of surfactants. The prevention of the action of microorganisms can be brought about by various antibacterial ad antifungal agents, for example, parabens, chlorobutanol, phenol, sorbic acid, thimerosal, and the like. In many cases, it will be preferable to include isotonic agents, for example, sugars or sodium chloride. Prolonged absorption of the injectable compositions can be brought about by the use in the compositions of agents delaying absorption, for example, aluminum monostearate and gelatin.

For parenteral administration in an aqueous solution, for example, the solution should be suitably buffered if necessary and the liquid diluent first rendered isotonic with sufficient saline or glucose. These particular aqueous solutions are especially suitable for intravenous, intramuscular, subcutaneous and intraperitoneal administration. In this connection, a sterile aqueous medium that can be employed will be known to those of skill in the art in light of the present disclosure. For example, one dosage may be dissolved in 1 ml of isotonic NaCl solution and either added to 1000 ml of hypodermoclysis fluid or injected at the proposed site of infusion, (see for example, "Remington's Pharmaceutical Sciences" 15th Edition, pages 1035-1038 and 1570-1580). Some variation in dosage will necessarily occur depending on the condition of the subject being treated. The person responsible for administration will, in any event, determine the appropriate dose for the individual subject. Moreover, for human administration, preparations should meet sterility, pyrogenicity, and the general safety and purity standards as required by FDA Office of Biologics standards.

Sterile injectable solutions are prepared by incorporating the active compounds in the required amount in the appropriate solvent with various of the other ingredients enumerated above, as required, followed by filtered sterilization. Generally, dispersions are prepared by incorporating the various sterilized active ingredients into a sterile vehicle which contains the basic dispersion medium and the required other ingredients from those enumerated above. In the case of sterile powders for the preparation of sterile injectable solutions, the preferred methods of preparation are vacuum-drying and freeze-drying techniques which yield a powder of the active ingredient plus any additional desired ingredient from a previously sterile-filtered solution thereof.

The compositions disclosed herein may be formulated in a neutral or salt form. Pharmaceutically-acceptable salts, include the acid addition salts (formed with the free amino groups of the protein) and which are formed with inorganic acids such as, for example, hydrochloric or phosphoric acids, or such organic acids as acetic, oxalic, tartaric, mandelic, and the like. Salts formed with the free carboxyl groups can also be derived from inorganic bases such as, for example, sodium, potassium, ammonium, calcium, or ferric hydroxides, and such organic bases as isopropylamine,

trimethylamine, histidine, procaine and the like. Upon formulation, solutions will be administered in a manner compatible with the dosage formulation and in such amount as is therapeutically effective. The formulations are easily administered in a variety of dosage forms such as injectable solutions, drug-release capsules, and the like.

As used herein, "carrier" includes any and all solvents, dispersion media, vehicles, coatings, diluents, antibacterial and antifungal agents, isotonic and absorption delaying agents, buffers, carrier solutions, suspensions, colloids, and the like. The use of such media and agents for pharmaceutical active substances is well known in the art. Except insofar as any conventional media or agent is incompatible with the active ingredient, its use in the therapeutic compositions is contemplated. Supplementary active ingredients can also be incorporated into the compositions.

The phrase "pharmaceutically-acceptable" refers to molecular entities and compositions that do not produce an allergic or similar untoward reaction when administered to a mammal, and in particular, when administered to a human. The preparation of an aqueous composition that contains a protein as an active ingredient is well understood in the art. Typically, such compositions are prepared as injectables, either as liquid solutions or suspensions; solid forms suitable for solution in, or suspension in, liquid prior to injection can also be prepared. The preparation can also be emulsified. In certain embodiments, the compositions of the present invention may be formulated for topical, or transdermal delivery to one or more tissue sites or cell types within the body of the vertebrate being treated. Alternatively, in the embodiments where *ex vivo* or *ex situ* modalities are preferred, the compositions of the invention my be used externally from the body of the intended recipient by first contacting a cell suspension or a tissue sample, or other extracorporeal composition with the compositions to facilitate transfer of the viral vectors into the cells or tissues in *ex vivo* fashion. Following suitable transfection, then, such cells or tissues could be reintroduced into the body of the animal being treated.

4.21 LIPOSOME-, NANOCAPSULE-, AND MICROPARTICLE-MEDIATED DELIVERY

In certain embodiments, the genetic constructs of the present invention, and/or the virus particles or virions comprising them may further comprise one or more liposomes, nanocapsules, microparticles, microspheres, lipid particles, vesicles, and the like, for enhancing, facilitating, or increasing the effectiveness of introducing the gene therapy constructs of the present invention into suitable host cells, tissues, or organs. In particular, the addition of a lipid particle, a liposome, a vesicle, a nanosphere, or a nanoparticle or the like to the compositions of the invention may serve to enhance or facilitate the delivery of the vectors, virions, or virus particles into the target cells or tissues.

Such formulations may be preferred for the introduction of pharmaceutically acceptable formulations of the nucleic acids or the gene expression cassettes and viral vector constructs disclosed herein. The formation and use of liposomes is generally known to those of skill in the art (see for example, Couvreur *et al.*, 1977; Couvreur, 1988; Lasic, 1998; which describes the use of liposomes and

nanocapsules in the targeted antibiotic therapy for intracellular bacterial infections and diseases). Recently, liposomes were developed with improved serum stability and circulation half-times (Gabizon and Papahadjopoulos, 1988; Allen and Choun, 1987; U. S. Patent 5,741,516, specifically incorporated herein by reference in its entirety). Further, various methods of liposome and liposome like preparations as potential drug carriers have been reviewed (Takakura, 1998; Chandran *et al.*, 1997; Margalit, 1995; U.S. Patent 5,567,434; U.S. Patent 5,552,157; U.S. Patent 5,565,213; U.S. Patent 5,738,868 and U.S. Patent 5,795,587, each specifically incorporated herein by reference in its entirety).

Liposomes have been used successfully with a number of cell types that are normally resistant to transfection by other procedures including T cell suspensions, primary hepatocyte cultures and PC 12 cells (Renneisen *et al.*, 1990; Muller *et al.*, 1990). In addition, liposomes are free of the DNA length constraints that are typical of viral-based delivery systems. Liposomes have been used effectively to introduce genes, drugs (Heath and Martin, 1986; Heath *et al.*, 1986; Balazsovits *et al.*, 1989; Fresta and Puglisi, 1996), radiotherapeutic agents (Pikul *et al.*, 1987), enzymes (Imaizumi *et al.*, 1990a; Imaizumi *et al.*, 1990b), viruses (Faller and Baltimore, 1984), transcription factors and allosteric effectors (Nicolau and Gersonde, 1979) into a variety of cultured cell lines and animals. In addition, several successful clinical trails examining the effectiveness of liposome-mediated drug delivery have been completed (Lopez-Berestein *et al.*, 1985a; 1985b; Coune, 1988; Sculier *et al.*, 1988). Furthermore, several studies suggest that the use of liposomes is not associated with autoimmune responses, toxicity or gonadal localization after systemic delivery (Mori and Fukatsu, 1992).

Liposomes are formed from phospholipids that are dispersed in an aqueous medium and spontaneously form multilamellar concentric bilayer vesicles (also termed multilamellar vesicles (MLVs). MLVs generally have diameters of from 25 nm to 4 μm. Sonication of MLVs results in the formation of small unilamellar vesicles (SUVs) with diameters in the range of 200 to 500 Å, containing an aqueous solution in the core.

Liposomes bear resemblance to cellular membranes and are contemplated for use in connection with the present invention as carriers for the peptide compositions. They are widely suitable as both water- and lipid-soluble substances can be entrapped, *i.e.* in the aqueous spaces and within the bilayer itself, respectively. It is possible that the drug-bearing liposomes may even be employed for site-specific delivery of active agents by selectively modifying the liposomal formulation.

In addition to the teachings of Couvreur *et al.* (1977; 1980), the following information may be utilized in generating liposomal formulations. Phospholipids can form a variety of structures other than liposomes when dispersed in water, depending on the molar ratio of lipid to water. At low ratios the liposome is the preferred structure. The physical characteristics of liposomes depend on pH, ionic strength and the presence of divalent cations. Liposomes can show low permeability to ionic and polar substances, but at elevated temperatures undergo a phase transition which markedly alters their

permeability. The phase transition involves a change from a closely packed, ordered structure, known as the gel state, to a loosely packed, less-ordered structure, known as the fluid state. This occurs at a characteristic phase-transition temperature and results in an increase in permeability to ions, sugars and drugs.

In addition to temperature, exposure to proteins can alter the permeability of liposomes. Certain soluble proteins, such as cytochrome c, bind, deform and penetrate the bilayer, thereby causing changes in permeability. Cholesterol inhibits this penetration of proteins, apparently by packing the phospholipids more tightly. It is contemplated that the most useful liposome formations for antibiotic and inhibitor delivery will contain cholesterol.

The ability to trap solutes varies between different types of liposomes. For example, MLVs are moderately efficient at trapping solutes, but SUVs are extremely inefficient. SUVs offer the advantage of homogeneity and reproducibility in size distribution, however, and a compromise between size and trapping efficiency is offered by large unilamellar vesicles (LUVs). These are prepared by ether evaporation and are three to four times more efficient at solute entrapment than MLVs.

In addition to liposome characteristics, an important determinant in entrapping compounds is the physicochemical properties of the compound itself. Polar compounds are trapped in the aqueous spaces and nonpolar compounds bind to the lipid bilayer of the vesicle. Polar compounds are released through permeation or when the bilayer is broken, but nonpolar compounds remain affiliated with the bilayer unless it is disrupted by temperature or exposure to lipoproteins. Both types show maximum efflux rates at the phase transition temperature.

Liposomes interact with cells *via* four different mechanisms: Endocytosis by phagocytic cells of the reticuloendothelial system such as macrophages and neutrophils; adsorption to the cell surface, either by nonspecific weak hydrophobic or electrostatic forces, or by specific interactions with cell-surface components; fusion with the plasma cell membrane by insertion of the lipid bilayer of the liposome into the plasma membrane, with simultaneous release of liposomal contents into the cytoplasm; and by transfer of liposomal lipids to cellular or subcellular membranes, or *vice versa*, without any association of the liposome contents. It often is difficult to determine which mechanism is operative and more than one may operate at the same time.

The fate and disposition of intravenously injected liposomes depend on their physical properties, such as size, fluidity, and surface charge. They may persist in tissues for h or days, depending on their composition, and half lives in the blood range from min to several h. Larger liposomes, such as MLVs and LUVs, are taken up rapidly by phagocytic cells of the reticuloendothelial system, but physiology of the circulatory system restrains the exit of such large species at most sites. They can exit only in places where large openings or pores exist in the capillary endothelium, such as the sinusoids of the liver or spleen. Thus, these organs are the predominate site of uptake. On the

other hand, SUVs show a broader tissue distribution but still are sequestered highly in the liver and spleen. In general, this *in vivo* behavior limits the potential targeting of liposomes to only those organs and tissues accessible to their large size. These include the blood, liver, spleen, bone marrow, and lymphoid organs.

Alternatively, the invention provides for pharmaceutically acceptable nanocapsule formulations of the compositions of the present invention. Nanocapsules can generally entrap compounds in a stable and reproducible way (Henry-Michelland *et al.*, 1987; Quintanar-Guerrero *et al.*, 1998; Douglas *et al.*, 1987). To avoid side effects due to intracellular polymeric overloading, such ultrafine particles (sized around 0.1 μm) should be designed using polymers able to be degraded *in vivo*. Biodegradable polyalkyl-cyanoacrylate nanoparticles that meet these requirements are contemplated for use in the present invention. Such particles may be are easily made, as described (Couvreur *et al.*, 1980; Couvreur, 1988; zur Muhlen *et al.*, 1998; Zambaux *et al.* 1998; Pinto-Alphandry *et al.*, 1995 and U. S. Patent 5,145,684, specifically incorporated herein by reference in its entirety).

4.22 THERAPEUTIC AND DIAGNOSTIC KITS

The invention also encompasses one or more polynucleotide compositions together with one or more pharmaceutically-acceptable excipients, carriers, diluents, adjuvants, and/or other components, as may be employed in the formulation of particular viral vector formulations, and in the preparation of therapeutic agents for administration to a mammal, and in particularly, to a human, for one or more of the indications described herein for which viral vector-based gene therapy provides an alternative to current treatment modalities. In particular, such kits may comprise one or more viral vector compositions that comprise at least a first gene expression cassette in combination with instructions for using the viral vector in the treatment of such disorders in a mammal, and may typically further include containers prepared for convenient commercial packaging.

As such, preferred animals for administration of the pharmaceutical compositions disclosed herein include mammals, and particularly humans. Other preferred animals include murines, bovines, equines, porcines, canines, and felines. The composition may include partially or significantly purified gene expression cassette-comprising viral vector compositions, either alone, or in combination with one or more additional active ingredients, which may be obtained from natural or recombinant sources, or which may be obtainable naturally or either chemically synthesized, or alternatively produced *in vitro* from recombinant host cells expressing DNA segments encoding such additional active ingredients.

Therapeutic kits may also be prepared that comprise at least one of the compositions disclosed herein and instructions for using the composition as a therapeutic agent. The container means for such kits may typically comprise at least one vial, test tube, flask, bottle, syringe or other container means,

into which the disclosed genetic composition(s) may be placed, and preferably suitably aliquoted. Where a second therapeutic composition is also provided, the kit may also contain a second distinct container means into which this second composition may be placed. Alternatively, the plurality of therapeutic compositions may be prepared in a single pharmaceutical composition, and may be packaged in a single container means, such as a vial, flask, syringe, bottle, or other suitable single container means. The kits of the present invention will also typically include a means for containing the vial(s) in close confinement for commercial sale, such as, *e.g.*, injection or blow-molded plastic containers into which the desired vial(s) are retained.

4.23 METHODS OF NUCLEIC ACID DELIVERY AND DNA TRANSFECTION

In certain embodiments, it is contemplated that one or more of the viral vector-delivered therapeutic product-encoding RNA, DNA, PNAs and/or substituted polynucleotide compositions disclosed herein will be used to transfect an appropriate host cell. Technology for introduction of viral vectors comprising one or more PNAs, RNAs, and DNAs into target host cells is well known to those of skill in the art.

Several non-viral methods for the transfer of expression constructs into cultured mammalian cells also are contemplated by the present invention for use in certain *in vitro* embodiments, and under conditions where the use of viral vector-mediated delivery is less desirable. These include calcium phosphate precipitation (Graham and Van Der Eb, 1973; Chen and Okayama, 1987; Rippe *et al.*, 1990) DEAE-dextran (Gopal, 1985), electroporation (Wong and Neumann, 1982; Fromm *et al.*, 1985; Tur-Kaspa *et al.*, 1986; Potter *et al.*, 1984; Suzuki et al., 1998; Vanbever *et al.*, 1998), direct microinjection (Capecchi, 1980; Harland and Weintraub, 1985), DNA-loaded liposomes (Nicolau and Sene, 1982; Fraley *et al.*, 1979; Takakura, 1998) and lipofectamine-DNA complexes, cell sonication (Fechheimer *et al.*, 1987), gene bombardment using high velocity microprojectiles (Yang *et al.*, 1990; Klein *et al.*, 1992), and receptor-mediated transfection (Curiel *et al.*, 1991; Wagner *et al.*, 1992; Wu and Wu, 1987; Wu and Wu, 1988). Some of these techniques may be successfully adapted for *in vivo* or *ex vivo* use.

4.24 EXPRESSION IN ANIMAL CELLS

The inventors contemplate that the expression cassettes of the present invention that comprise one or more contiguous nucleic acid sequences that encodes a therapeutic agent of the present invention may be utilized to treat one or more cellular defects in a host cell that comprises the vector. Such cells are preferably animal cells, including mammalian cells such as those obtained from a human or other primates, murine, canine, feline, ovine, caprine, bovine, equine, epine, or porcine species. In particular, the use of such constructs for the treatment and/or amelioration of disorders, dysfunctions, and diseases in a human subject suspected of suffering from such a condition is highly contemplated. The cells may be transformed with one or more viral vectors comprising one or more of the disclosed

expression constructs, such that the encoded therapeutic agent is introduced into and expressed in the host cells of the animal is sufficient to alter, reduce, ameliorate or prevent the deleterious or disease conditions either *in vitro* and/or *in vivo*.

4.25 SITE-SPECIFIC MUTAGENESIS

Site-specific mutagenesis is a technique useful in the preparation of individual peptides, or biologically functional equivalent polypeptides, through specific mutagenesis of the underlying polynucleotides that encode them. The technique, well-known to those of skill in the art, further provides a ready ability to prepare and test sequence variants, for example, incorporating one or more of the foregoing considerations, by introducing one or more nucleotide sequence changes into the DNA. Site-specific mutagenesis allows the production of mutants through the use of specific oligonucleotide sequences which encode the DNA sequence of the desired mutation, as well as a sufficient number of adjacent nucleotides, to provide a primer sequence of sufficient size and sequence complexity to form a stable duplex on both sides of the deletion junction being traversed. Mutations may be employed in a selected polynucleotide sequence to improve, alter, decrease, modify, or change the properties of the polynucleotide itself, and/or alter the properties, activity, composition, stability, or primary sequence of the encoded polypeptide.

In certain embodiments of the present invention, the inventors contemplate the mutagenesis of the disclosed genetic constructs to alter the activity or effectiveness of such constructs in increasing or altering their therapeutic activity, or to effect higher or more desirable introduction in a particular host cell or tissue. Likewise in certain embodiments, the inventors contemplate the mutagenesis of the therapeutic genes comprised in such viral vectors themselves, or of the viral vector delivery vehicle to facilitate improved regulation of the particular therapeutic construct's activity, solubility, stability, expression, or efficacy *in vitro, in situ,* and/or *in vivo.*

The techniques of site-specific mutagenesis are well known in the art, and are widely used to create variants of both polypeptides and polynucleotides. For example, site-specific mutagenesis is often used to alter a specific portion of a DNA molecule. In such embodiments, a primer comprising typically about 14 to about 25 nucleotides or so in length is employed, with about 5 to about 10 residues on both sides of the junction of the sequence being altered.

As will be appreciated by those of skill in the art, site-specific mutagenesis techniques have often employed a phage vector that exists in both a single stranded and double stranded form. Typical vectors useful in site-directed mutagenesis include vectors such as the M13 phage. These phage are readily commercially-available and their use is generally well-known to those skilled in the art. Double-stranded plasmids are also routinely employed in site directed mutagenesis that eliminates the step of transferring the gene of interest from a plasmid to a phage.

In general, site-directed mutagenesis in accordance herewith is performed by first obtaining a single-stranded vector or melting apart of two strands of a double-stranded vector that includes within its sequence a DNA sequence that encodes the desired peptide. An oligonucleotide primer bearing the desired mutated sequence is prepared, generally synthetically. This primer is then annealed with the single-stranded vector, and subjected to DNA polymerizing enzymes such as *E. coli* polymerase I Klenow fragment, in order to complete the synthesis of the mutation-bearing strand. Thus, a heteroduplex is formed wherein one strand encodes the original non-mutated sequence and the second strand bears the desired mutation. This heteroduplex vector is then used to transform appropriate cells, such as *E. coli* cells, and clones are selected which include recombinant vectors bearing the mutated sequence arrangement.

The preparation of sequence variants of the selected peptide-encoding DNA segments using site-directed mutagenesis provides a means of producing potentially useful species and is not meant to be limiting as there are other ways in which sequence variants of peptides and the DNA sequences encoding them may be obtained. For example, recombinant vectors encoding the desired peptide sequence may be treated with mutagenic agents, such as hydroxylamine, to obtain sequence variants. Specific details regarding these methods and protocols are found in the teachings of Maloy *et al.*, 1994; Segal, 1976; Prokop and Bajpai, 1991; Kuby, 1994; and Maniatis *et al.*, 1982, each incorporated herein by reference, for that purpose.

As used herein, the term "oligonucleotide directed mutagenesis procedure" refers to template-dependent processes and vector-mediated propagation that result in an increase in the concentration of a specific nucleic acid molecule relative to its initial concentration, or in an increase in the concentration of a detectable signal, such as amplification. As used herein, the term "oligonucleotide directed mutagenesis procedure" is intended to refer to a process that involves the template-dependent extension of a primer molecule. The term template dependent process refers to nucleic acid synthesis of an RNA or a DNA molecule wherein the sequence of the newly synthesized strand of nucleic acid is dictated by the well-known rules of complementary base pairing. Typically, vector mediated methodologies involve the introduction of the nucleic acid fragment into a DNA or RNA vector, the clonal amplification of the vector, and the recovery of the amplified nucleic acid fragment. Examples of such methodologies are provided by U. S. Patent No. 4,237,224, specifically incorporated herein by reference in its entirety.

A number of template dependent processes are available to amplify the target sequences of interest present in a sample. One of the best known amplification methods is the polymerase chain reaction (PCR™) which is described in detail in U.S. Patent Nos. 4,683,195, 4,683,202 and 4,800,159, each of which is incorporated herein by reference in its entirety. Briefly, in PCR™, two primer sequences are prepared which are complementary to regions on opposite complementary strands of the target sequence. An excess of deoxynucleoside triphosphates is added to a reaction mixture along with

a DNA polymerase (e.g., *Taq* polymerase). If the target sequence is present in a sample, the primers will bind to the target and the polymerase will cause the primers to be extended along the target sequence by adding on nucleotides. By raising and lowering the temperature of the reaction mixture, the extended primers will dissociate from the target to form reaction products, excess primers will bind to the target and to the reaction product and the process is repeated. Preferably reverse transcription and PCR™ amplification procedure may be performed in order to quantify the amount of mRNA amplified. Polymerase chain reaction methodologies are well known in the art.

Another method for amplification is the ligase chain reaction (referred to as LCR), disclosed in Eur. Pat. Appl. Publ. No. 320,308 (specifically incorporated herein by reference in its entirety). In LCR, two complementary probe pairs are prepared, and in the presence of the target sequence, each pair will bind to opposite complementary strands of the target such that they abut. In the presence of a ligase, the two probe pairs will link to form a single unit. By temperature cycling, as in PCR™, bound ligated units dissociate from the target and then serve as "target sequences" for ligation of excess probe pairs. U. S. Patent No. 4,883,750, incorporated herein by reference in its entirety, describes an alternative method of amplification similar to LCR for binding probe pairs to a target sequence.

Qbeta Replicase, described in PCT Intl. Pat. Appl. Publ. No. PCT/US87/00880, incorporated herein by reference in its entirety, may also be used as still another amplification method in the present invention. In this method, a replicative sequence of RNA that has a region complementary to that of a target is added to a sample in the presence of an RNA polymerase. The polymerase will copy the replicative sequence that can then be detected.

An isothermal amplification method, in which restriction endonucleases and ligases are used to achieve the amplification of target molecules that contain nucleotide 5'-[α-thio]triphosphates in one strand of a restriction site (Walker *et al.*, 1992), may also be useful in the amplification of nucleic acids in the present invention.

Strand Displacement Amplification (SDA) is another method of carrying out isothermal amplification of nucleic acids that involves multiple rounds of strand displacement and synthesis, *i.e.* nick translation. A similar method, called Repair Chain Reaction (RCR) is another method of amplification which may be useful in the present invention and is involves annealing several probes throughout a region targeted for amplification, followed by a repair reaction in which only two of the four bases are present. The other two bases can be added as biotinylated derivatives for easy detection. A similar approach is used in SDA.

Sequences can also be detected using a cyclic probe reaction (CPR). In CPR, a probe having a 3' and 5' sequences of non-target DNA and an internal or "middle" sequence of the target protein specific RNA is hybridized to DNA which is present in a sample. Upon hybridization, the reaction is treated with RNaseH, and the products of the probe are identified as distinctive products by generating a signal that is released after digestion. The original template is annealed to another cycling probe and

the reaction is repeated. Thus, CPR involves amplifying a signal generated by hybridization of a probe to a target gene specific expressed nucleic acid.

Still other amplification methods described in Great Britain Pat. Appl. No. 2 202 328, and in PCT Intl. Pat. Appl. Publ. No. PCT/US89/01025, each of which is incorporated herein by reference in its entirety, may be used in accordance with the present invention. In the former application, "modified" primers are used in a PCR-like, template and enzyme dependent synthesis. The primers may be modified by labeling with a capture moiety (*e.g.,* biotin) and/or a detector moiety (*e.g.,* enzyme). In the latter application, an excess of labeled probes is added to a sample. In the presence of the target sequence, the probe binds and is cleaved catalytically. After cleavage, the target sequence is released intact to be bound by excess probe. Cleavage of the labeled probe signals the presence of the target sequence.

Other nucleic acid amplification procedures include transcription-based amplification systems (TAS) (Kwoh *et al.,* 1989; PCT Intl. Pat. Appl. Publ. No. WO 88/10315, incorporated herein by reference in its entirety), including nucleic acid sequence based amplification (NASBA) and 3SR. In NASBA, the nucleic acids can be prepared for amplification by standard phenol/chloroform extraction, heat denaturation of a sample, treatment with lysis buffer and minispin columns for isolation of DNA and RNA or guanidinium chloride extraction of RNA. These amplification techniques involve annealing a primer that has sequences specific to the target sequence. Following polymerization, DNA/RNA hybrids are digested with RNase H while double stranded DNA molecules are heat-denatured again. In either case the single stranded DNA is made fully double stranded by addition of second target-specific primer, followed by polymerization. The double stranded DNA molecules are then multiply transcribed by a polymerase such as T7 or SP6. In an isothermal cyclic reaction, the RNAs are reverse transcribed into DNA, and transcribed once again with a polymerase such as T7 or SP6. The resulting products, whether truncated or complete, indicate target-specific sequences.

Eur. Pat. Appl. Publ. No. 329,822, incorporated herein by reference in its entirety, disclose a nucleic acid amplification process involving cyclically synthesizing single-stranded RNA ("ssRNA"), ssDNA, and double-stranded DNA (dsDNA), which may be used in accordance with the present invention. The ssRNA is a first template for a first primer oligonucleotide, which is elongated by reverse transcriptase (RNA-dependent DNA polymerase). The RNA is then removed from resulting DNA:RNA duplex by the action of ribonuclease H (RNase H, an RNase specific for RNA in a duplex with either DNA or RNA). The resultant ssDNA is a second template for a second primer, which also includes the sequences of an RNA polymerase promoter (exemplified by T7 RNA polymerase) 5' to its homology to its template. This primer is then extended by DNA polymerase (exemplified by the large "Klenow" fragment of *E. coli* DNA polymerase I), resulting as a double-stranded DNA ("dsDNA") molecule, having a sequence identical to that of the original RNA between the primers and having additionally, at one end, a promoter sequence. This promoter sequence can be used by the appropriate

RNA polymerase to make many RNA copies of the DNA. These copies can then re-enter the cycle leading to very swift amplification. With proper choice of enzymes, this amplification can be done isothermally without addition of enzymes at each cycle. Because of the cyclical nature of this process, the starting sequence can be chosen to be in the form of either DNA or RNA.

PCT Intl. Pat. Appl. Publ. No. WO 89/06700, incorporated herein by reference in its entirety, disclose a nucleic acid sequence amplification scheme based on the hybridization of a promoter/primer sequence to a target single-stranded DNA ("ssDNA") followed by transcription of many RNA copies of the sequence. This scheme is not cyclic; i.e. new templates are not produced from the resultant RNA transcripts. Other amplification methods include "RACE" (Frohman, 1990), and "one-sided PCR" (Ohara *et al.,* 1989) which are well-known to those of skill in the art.

Methods based on ligation of two (or more) oligonucleotides in the presence of nucleic acid having the sequence of the resulting "di-oligonucleotide", thereby amplifying the di-oligonucleotide (Wu and Dean, 1996, incorporated herein by reference in its entirety), may also be used in the amplification of DNA sequences of the present invention.

4.26 BIOLOGICAL FUNCTIONAL EQUIVALENTS

Modification and changes may be made in the structure of the gene expression cassettes, or to the viral vectors comprising them, as well as modification to the the therapeutic agents encoded by them and still obtain functional vectors, viral particles, and virion that encode one or more therapeutic agents with desirable characteristics. As mentioned above, it is often desirable to introduce one or more mutations into a specific polynucleotide sequence. In certain circumstances, the resulting encoded polypeptide sequence is altered by this mutation, or in other cases, the sequence of the polypeptide is unchanged by one or more mutations in the encoding polynucleotide.

When it is desirable to alter the amino acid sequence of a polypeptide to create an equivalent, or even an improved, second-generation molecule, the amino acid changes may be achieved by changing one or more of the codons of the encoding DNA sequence, according to Table 3.

For example, certain amino acids may be substituted for other amino acids in a protein structure without appreciable loss of interactive binding capacity with structures such as, for example, antigen-binding regions of antibodies or binding sites on substrate molecules. Since it is the interactive capacity and nature of a protein that defines that protein's biological functional activity, certain amino acid sequence substitutions can be made in a protein sequence, and, of course, its underlying DNA coding sequence, and nevertheless obtain a protein with like properties. It is thus contemplated by the inventors that various changes may be made in the peptide sequences of the disclosed compositions, or corresponding DNA sequences which encode said peptides without appreciable loss of their biological utility or activity.

TABLE 3

AMINO ACIDS		CODONS						
Alanine	Ala	A	GCA	GCC	GCG	GCU		
Cysteine	Cys	C	UGC	UGU				
Aspartic acid	Asp	D	GAC	GAU				
Glutamic acid	Glu	E	GAA	GAG				
Phenylalanine	Phe	F	UUC	UUU				
Glycine	Gly	G	GGA	GGC	GGG	GGU		
Histidine	His	H	CAC	CAU				
Isoleucine	Ile	I	AUA	AUC	AUU			
Lysine	Lys	K	AAA	AAG				
Leucine	Leu	L	UUA	UUG	CUA	CUC	CUG	CUU
Methionine	Met	M	AUG					
Asparagine	Asn	N	AAC	AAU				
Proline	Pro	P	CCA	CCC	CCG	CCU		
Glutamine	Gln	Q	CAA	CAG				
Arginine	Arg	R	AGA	AGG	CGA	CGC	CGG	CGU
Serine	Ser	S	AGC	AGU	UCA	UCC	UCG	UCU
Threonine	Thr	T	ACA	ACC	ACG	ACU		
Valine	Val	V	GUA	GUC	GUG	GUU		
Tryptophan	Trp	W	UGG					
Tyrosine	Tyr	Y	UAC	UAU				

In making such changes, the hydropathic index of amino acids may be considered. The importance of the hydropathic amino acid index in conferring interactive biologic function on a protein is generally understood in the art (Kyte and Doolittle, 1982, incorporate herein by reference). It is accepted that the relative hydropathic character of the amino acid contributes to the secondary structure of the resultant protein, which in turn defines the interaction of the protein with other molecules, for example, enzymes, substrates, receptors, DNA, antibodies, antigens, and the like. Each amino acid has been assigned a hydropathic index on the basis of its hydrophobicity and charge characteristics (Kyte and Doolittle, 1982). These values are: isoleucine (+4.5); valine (+4.2); leucine (+3.8); phenylalanine (+2.8); cysteine/cystine (+2.5); methionine (+1.9); alanine (+1.8); glycine (–0.4); threonine (–0.7); serine (–0.8); tryptophan (–0.9); tyrosine (–1.3); proline (–1.6); histidine (–3.2); glutamate (–3.5); glutamine (–3.5); aspartate (–3.5); asparagine (–3.5); lysine (–3.9); and arginine (–4.5).

It is known in the art that certain amino acids may be substituted by other amino acids having a similar hydropathic index or score and still result in a protein with similar biological activity, *i.e.* still

obtain a biological functionally equivalent protein. In making such changes, the substitution of amino acids whose hydropathic indices are within ±2 is preferred, those within ±1 are particularly preferred, and those within ±0.5 are even more particularly preferred. It is also understood in the art that the substitution of like amino acids can be made effectively on the basis of hydrophilicity. U. S. Patent 4,554,101 (specifically incorporated herein by reference in its entirety), states that the greatest local average hydrophilicity of a protein, as governed by the hydrophilicity of its adjacent amino acids, correlates with a biological property of the protein.

As detailed in U. S. Patent 4,554,101, the following hydrophilicity values have been assigned to amino acid residues: arginine (+3.0); lysine (+3.0); aspartate (+3.0 ± 1); glutamate (+3.0 ± 1); serine (+0.3); asparagine (+0.2); glutamine (+0.2); glycine (0); threonine (–0.4); proline (–0.5 ± 1); alanine (–0.5); histidine (–0.5); cysteine (–1.0); methionine (–1.3); valine (–1.5); leucine (–1.8); isoleucine (–1.8); tyrosine (–2.3); phenylalanine (–2.5); tryptophan (–3.4). It is understood that an amino acid can be substituted for another having a similar hydrophilicity value and still obtain a biologically equivalent, and in particular, an immunologically equivalent protein. In such changes, the substitution of amino acids whose hydrophilicity values are within ±2 is preferred, those within ±1 are particularly preferred, and those within ±0.5 are even more particularly preferred.

As outlined above, amino acid substitutions are generally therefore based on the relative similarity of the amino acid side-chain substituents, for example, their hydrophobicity, hydrophilicity, charge, size, and the like. Exemplary substitutions that take various of the foregoing characteristics into consideration are well known to those of skill in the art and include: arginine and lysine; glutamate and aspartate; serine and threonine; glutamine and asparagine; and valine, leucine and isoleucine.

4.27 RIBOZYMES

In certain embodiments, aspects of the invention concerns the use of the genetic expression constructs and gene expression cassettes to deliver catalytic RNA molecules (ribozymes) to selected mammalian cells and tissues to effect a reduction or elimination of expression of one or more native DNA or mRNA molecules, so as to prevent or reduce the amount of the translation product of such mRNAs. Ribozymes are biological catalysts consisting of only RNA. They promote a variety of reactions involving RNA and DNA molecules including site-specific cleavage, ligation, polymerization, and phosphoryl exchange (Cech, 1989; Cech, 1990). Ribozymes fall into three broad classes: (1) RNAse P, (2) self-splicing introns, and (3) self-cleaving viral agents. Self-cleaving agents include hepatitis delta virus and components of plant virus satellite RNAs that sever the RNA genome as part of a rolling-circle mode of replication. Because of their small size and great specificity, ribozymes have the greatest potential for biotechnical applications. The ability of ribozymes to cleave other RNA molecules at specific sites in a catalytic manner has brought them into consideration as

inhibitors of viral replication or of cell proliferation and gives them potential advantage over antisense RNA. Indeed, ribozymes have already been used to cleave viral targets and oncogene products in living cells (Koizumi *et al.*, 1992; Kashani-Sabet *et al.*, 1992; Taylor and Rossi, 1991; von-Weizsacker *et al.*, 1992; Ojwang *et al.*, 1992; Stephenson and Gibson, 1991; Yu *et al.*, 1993; Xing and Whitton, 1993; Yu *et al.*, 1995; Little and Lee, 1995).

Two kinds of ribozymes have been employed widely, hairpins and hammerheads. Both catalyze sequence-specific cleavage resulting in products with a 5N hydroxyl and a 2N,3N-cyclic phosphate. Hammerhead ribozymes have been used more commonly, because they impose few restrictions on the target site. Hairpin ribozymes are more stable and, consequently, function better than hammerheads at physiologic temperature and magnesium concentrations.

A number of patents have issued describing various ribozymes and methods for designing ribozymes. See, for example, U.S. Patent Nos. 5,646,031; 5,646,020; 5,639,655; 5,093,246; 4,987,071; 5,116,742; and 5,037,746, each specifically incorporated herein by reference in its entirety. However, the ability of ribozymes to provide therapeutic benefit *in vivo* has not yet been demonstrated.

Although proteins traditionally have been used for catalysis of nucleic acids, another class of macromolecules has emerged as useful in this endeavor. Ribozymes are RNA-protein complexes that cleave nucleic acids in a site-specific fashion. Ribozymes have specific catalytic domains that possess endonuclease activity (Kim and Cech, 1987; Gerlach *et al.*, 1987; Forster and Symons, 1987). For example, a large number of ribozymes accelerate phosphoester transfer reactions with a high degree of specificity, often cleaving only one of several phosphoesters in an oligonucleotide substrate (Cech *et al.*, 1981; Michel and Westhof, 1990; Reinhold-Hurek and Shub, 1992). This specificity has been attributed to the requirement that the substrate bind *via* specific base-pairing interactions to the internal guide sequence ("IGS") of the ribozyme prior to chemical reaction.

Ribozyme catalysis has primarily been observed as part of sequence-specific cleavage/ligation reactions involving nucleic acids (Joyce, 1989; Cech *et al.*, 1981). For example, U. S. Patent No. 5,354,855 (specifically incorporated herein by reference) reports that certain ribozymes can act as endonucleases with a sequence-specificity greater than that of known ribonucleases and approaching that of the DNA restriction enzymes. Thus, sequence-specific ribozyme-mediated inhibition of gene expression may be particularly suited to therapeutic applications (Scanlon *et al.*, 1991; Sarver *et al.*, 1990). Recently, it was reported that ribozymes elicited genetic changes in some cells lines to which they were applied; the altered genes included the oncogenes H-*ras*, c-*fos* and genes of HIV. Most of this work involved the modification of a target mRNA, based on a specific mutant codon that is cleaved by a specific ribozyme.

Six basic varieties of naturally occurring enzymatic RNAs are known presently. Each can catalyze the hydrolysis of RNA phosphodiester bonds *in trans* (and thus can cleave other RNA molecules) under physiological conditions. In general, enzymatic nucleic acids act by first binding to a

target RNA. Such binding occurs through the target binding portion of a enzymatic nucleic acid which is held in close proximity to an enzymatic portion of the molecule that acts to cleave the target RNA. Thus, the enzymatic nucleic acid first recognizes and then binds a target RNA through complementary base pairing, and once bound to the correct site, acts enzymatically to cut the target RNA. Strategic cleavage of such a target RNA will destroy its ability to direct synthesis of an encoded protein. After an enzymatic nucleic acid has bound and cleaved its RNA target, it is released from that RNA to search for another target and can repeatedly bind and cleave new targets.

The enzymatic nature of a ribozyme is advantageous over many technologies, such as antisense technology (where a nucleic acid molecule simply binds to a nucleic acid target to block its translation) since the concentration of ribozyme necessary to affect a therapeutic treatment is lower than that of an antisense oligonucleotide. This advantage reflects the ability of the ribozyme to act enzymatically. Thus, a single ribozyme molecule is able to cleave many molecules of target RNA. In addition, the ribozyme is a highly specific inhibitor, with the specificity of inhibition depending not only on the base pairing mechanism of binding to the target RNA, but also on the mechanism of target RNA cleavage. Single mismatches, or base-substitutions, near the site of cleavage can completely eliminate catalytic activity of a ribozyme. Similar mismatches in antisense molecules do not prevent their action (Woolf *et al.*, 1992). Thus, the specificity of action of a ribozyme is greater than that of an antisense oligonucleotide binding the same RNA site.

The enzymatic nucleic acid molecule may be formed in a hammerhead, hairpin, a hepatitis δ virus, group I intron or RNaseP RNA (in association with an RNA guide sequence) or Neurospora VS RNA motif. Examples of hammerhead motifs are described by Rossi *et al.* (1992). Examples of hairpin motifs are described by Hampel *et al.* (Eur. Pat. Appl. Publ. No. EP 0360257), Hampel and Tritz (1989), Hampel *et al.* (1990) and U. S. Patent 5,631,359 (specifically incorporated herein by reference). An example of the hepatitis δ virus motif is described by Perrotta and Been (1992); an example of the RNaseP motif is described by Guerrier-Takada *et al.* (1983); Neurospora VS RNA ribozyme motif is described by Collins (Saville and Collins, 1990; Saville and Collins, 1991; Collins and Olive, 1993); and an example of the Group I intron is described in U. S. Patent 4,987,071 (specifically incorporated herein by reference). All that is important in an enzymatic nucleic acid molecule of this invention is that it has a specific substrate binding site which is complementary to one or more of the target gene RNA regions, and that it have nucleotide sequences within or surrounding that substrate binding site which impart an RNA cleaving activity to the molecule. Thus the ribozyme constructs need not be limited to specific motifs mentioned herein.

In certain embodiments, it may be important to produce enzymatic cleaving agents that exhibit a high degree of specificity for the RNA of a desired target, such as one of the sequences disclosed herein. The enzymatic nucleic acid molecule is preferably targeted to a highly conserved sequence region of a target mRNA. Such enzymatic nucleic acid molecules can be delivered exogenously to

specific cells as required, although in preferred embodiments the ribozymes are expressed from DNA or RNA vectors that are delivered to specific cells.

Small enzymatic nucleic acid motifs (*e.g.*, of the hammerhead or the hairpin structure) may also be used for exogenous delivery. The simple structure of these molecules increases the ability of the enzymatic nucleic acid to invade targeted regions of the mRNA structure. Alternatively, catalytic RNA molecules can be expressed within cells from eukaryotic promoters (*e.g.*, Scanlon *et al.*, 1991; Kashani-Sabet *et al.*, 1992; Dropulic *et al.*, 1992; Weerasinghe *et al.*, 1991; Ojwang *et al.*, 1992; Chen *et al.*, 1992; Sarver *et al.*, 1990). Those skilled in the art realize that any ribozyme can be expressed in eukaryotic cells from the appropriate DNA vector. The activity of such ribozymes can be augmented by their release from the primary transcript by a second ribozyme (Int. Pat. Appl. Publ. No. WO 93/23569, and Int. Pat. Appl. Publ. No. WO 94/02595, both hereby incorporated by reference; Ohkawa *et al.*, 1992; Taira *et al.*, 1991; and Ventura *et al.*, 1993).

Ribozymes may be added directly, or can be complexed with cationic lipids, lipid complexes, packaged within liposomes, or otherwise delivered to target cells. The RNA or RNA complexes can be locally administered to relevant tissues *ex vivo*, or *in vivo* through injection, aerosol inhalation, infusion pump or stent, with or without their incorporation in biopolymers.

Ribozymes may be designed as described in Int. Pat. Appl. Publ. No. WO 93/23569 and Int. Pat. Appl. Publ. No. WO 94/02595 (each specifically incorporated herein by reference) and synthesized to be tested *in vitro* and *in vivo*, as described. Such ribozymes can also be optimized for delivery. While specific examples are provided, those in the art will recognize that equivalent RNA targets in other species can be utilized when necessary.

Hammerhead or hairpin ribozymes may be individually analyzed by computer folding (Jaeger *et al.*, 1989) to assess whether the ribozyme sequences fold into the appropriate secondary structure, as described herein. Those ribozymes with unfavorable intramolecular interactions between the binding arms and the catalytic core are eliminated from consideration. Varying binding arm lengths can be chosen to optimize activity. Generally, at least 5 or so bases on each arm are able to bind to, or otherwise interact with, the target RNA.

Ribozymes of the hammerhead or hairpin motif may be designed to anneal to various sites in the mRNA message, and can be chemically synthesized. The method of synthesis used follows the procedure for normal RNA synthesis as described in Usman *et al.* (1987) and in Scaringe *et al.* (1990) and makes use of common nucleic acid protecting and coupling groups, such as dimethoxytrityl at the 5′-end, and phosphoramidites at the 3′-end. Average stepwise coupling yields are typically >98%. Hairpin ribozymes may be synthesized in two parts and annealed to reconstruct an active ribozyme (Chowrira and Burke, 1992). Ribozymes may be modified extensively to enhance stability by modification with nuclease resistant groups, for example, 2′-amino, 2′-C-allyl, 2′-flouro, 2′-o-methyl, 2′-H (for a review see *e.g.*, Usman and Cedergren, 1992). Ribozymes may be purified by gel

electrophoresis using general methods or by high-pressure liquid chromatography and resuspended in water.

Ribozyme activity can be optimized by altering the length of the ribozyme binding arms, or chemically synthesizing ribozymes with modifications that prevent their degradation by serum ribonucleases (see *e.g.*, Int. Pat. Appl. Publ. No. WO 92/07065; Perrault *et al*, 1990; Pieken *et al.*, 1991; Usman and Cedergren, 1992; Int. Pat. Appl. Publ. No. WO 93/15187; Int. Pat. Appl. Publ. No. WO 91/03162; Eur. Pat. Appl. Publ. No. 92110298.4; U.S. Patent 5,334,711; and Int. Pat. Appl. Publ. No. WO 94/13688, which describe various chemical modifications that can be made to the sugar moieties of enzymatic RNA molecules), modifications which enhance their efficacy in cells, and removal of stem II bases to shorten RNA synthesis times and reduce chemical requirements.

A preferred means of accumulating high concentrations of a ribozyme(s) within cells is to incorporate the ribozyme-encoding sequences into a DNA expression vector. Transcription of the ribozyme sequences are driven from a promoter for eukaryotic RNA polymerase I (pol I), RNA polymerase II (pol II), or RNA polymerase III (pol III). Transcripts from pol II or pol III promoters will be expressed at high levels in all cells; the levels of a given pol II promoter in a given cell type will depend on the nature of the gene regulatory sequences (enhancers, silencers, *etc.*) present nearby. Prokaryotic RNA polymerase promoters may also be used, providing that the prokaryotic RNA polymerase enzyme is expressed in the appropriate cells (Elroy-Stein and Moss, 1990; Gao and Huang, 1993; Lieber *et al.*, 1993; Zhou *et al.*, 1990). Ribozymes expressed from such promoters can function in mammalian cells (Kashani-Sabet *et al.*, 1992; Ojwang *et al.*, 1992; Chen *et al.*, 1992; Yu *et al.*, 1993; L'Huillier *et al.*, 1992; Lisziewicz *et al.*, 1993). Although incorporation of the present ribozyme constructs into adeno-associated viral vectors is preferred, such transcription units can be incorporated into a variety of vectors for introduction into mammalian cells, including but not restricted to, plasmid DNA vectors, other viral DNA vectors (such as adenovirus vectors), or viral RNA vectors (such as retroviral, semliki forest virus, sindbis virus vectors).

Sullivan *et al.* (Int. Pat. Appl. Publ. No. WO 94/02595) describes general methods for delivery of enzymatic RNA molecules. Ribozymes may be administered to cells by a variety of methods known to those familiar to the art, including, but not restricted to, encapsulation in liposomes, by iontophoresis, or by incorporation into other vehicles, such as hydrogels, cyclodextrins, biodegradable nanocapsules, and bioadhesive microspheres. For some indications, ribozymes may be directly delivered *ex vivo* to cells or tissues with or without the aforementioned vehicles. Alternatively, the RNA/vehicle combination may be locally delivered by direct inhalation, by direct injection or by use of a catheter, infusion pump or stent. Other routes of delivery include, but are not limited to, intravascular, intramuscular, subcutaneous or joint injection, aerosol inhalation, oral (tablet or pill form), topical, systemic, ocular, intraocular, retinal, subretinal, intraperitoneal, intracerebroventricular, intrathecal delivery, and/or direct injection to one or more tissues of the brain. More detailed

descriptions of ribozyme and rAAV vector delivery and administration are provided in Int. Pat. Appl. Publ. No. WO 94/02595 and Int. Pat. Appl. Publ. No. WO 93/23569, each specifically incorporated herein by reference.

Ribozymes and the AAV vectored-constructs of the present invention may be used to inhibit gene expression and define the role (essentially) of specified gene products in the progression of one or more neural diseases, dysfunctions, cancers,, and/or disorders. In this manner, other genetic targets may be defined as important mediators of the disease. These studies lead to better treatment of the disease progression by affording the possibility of combination therapies (*e.g.*, multiple ribozymes targeted to different genes, ribozymes coupled with known small molecule inhibitors, or intermittent treatment with combinations of ribozymes and/or other chemical or biological molecules).

4.28 ANTISENSE OLIGONUCLEOTIDES

In certain embodiments, the gene expression constructs of the invention, and the viral vectors comprising them will find utility in the delivery of one or more antisense oligonucleotides or polynucleotides for inhibiting the expression of a selected mammalian mRNA in a host cell that has been transformed with the construct.

In the art the letters, A, G, C, T, and U respectively indicate nucleotides in which the nucleoside is Adenosine (Ade), Guanosine (Gua), Cytidine (Cyt), Thymidine (Thy), and Uridine (Ura). As used in the specification and claims, compounds that are "antisense" to a particular PNA, DNA or mRNA "sense" strand are nucleotide compounds that have a nucleoside sequence that is complementary to the sense strand. It will be understood by those skilled in the art that the present invention broadly includes oligonucleotide compounds that are capable of binding to the selected DNA or mRNA sense strand. It will also be understood that mRNA includes not only the ribonucleotide sequences encoding a protein, but also regions including the 5'-untranslated region, the 3'-untranslated region, the 5'-cap region and the intron/exon junction regions.

The invention includes compounds which are not strictly antisense; the compounds of the invention also include those oligonucleotides that may have some bases that are not complementary to bases in the sense strand provided such compounds have sufficient binding affinity for the particular DNA or mRNA for which an inhibition of expression is desired. In addition, base modifications or the use of universal bases such as inosine in the oligonucleotides of the invention are contemplated within the scope of the subject invention.

The antisense compounds may have some or all of the phosphates in the nucleotides replaced by phosphorothioates (X=S) or methylphosphonates ($X=CH_3$) or other C_{1-4} alkylphosphonates. The antisense compounds optionally may be further differentiated from native DNA by replacing one or both of the free hydroxy groups of the antisense molecule with C_{1-4} alkoxy groups ($R=C_{1-4}$ alkoxy). As used herein, C_{1-4} alkyl means a branched or unbranched hydrocarbon having 1 to 4 carbon-atoms.

The disclosed antisense compounds also may be substituted at the 3′ and/or 5′ ends by a substituted acridine derivative. As used herein, "substituted acridine," means any acridine derivative capable of intercalating nucleotide strands such as DNA. Preferred substituted acridines are 2-methoxy-6-chloro-9-pentylaminoacridine, *N*-(6-chloro-2-methoxyacridinyl)-O-methoxydiisopropylaminophosphinyl-3-aminopropanol, and *N*-(6-chloro2-methoxyacridinyl)-O-methoxydiisopropylaminophosphinyl-5-aminopentanol. Other suitable acridine derivatives are readily apparent to persons skilled in the art. Additionally, as used herein "P(O)(O) -substituted acridine" means a phosphate covalently linked to a substitute acridine.

As used herein, the term "nucleotides" includes nucleotides in which the phosphate moiety is replaced by phosphorothioate or alkylphosphonate and the nucleotides may be substituted by substituted acridines.

In one embodiment, the antisense compounds of the invention differ from native DNA by the modification of the phosphodiester backbone to extend the life of the antisense molecule. For example, the phosphates can be replaced by phosphorothioates. The ends of the molecule may also be optimally substituted by an acridine derivative that intercalates nucleotide strands of DNA. Intl. Pat. Appl. Publ. No. WO 98/13526 and U. S. Patent 5,849,902 (each specifically incorporated herein by reference in its entirety) describe a method of preparing three component chimeric antisense compositions, and discuss many of the currently available methodologies for synthesis of substituted oligonucleotides having improved antisense characteristics and/or half-life.

The reaction scheme involves ^{1}H-tetrazole-catalyzed coupling of phosphoramidites to give phosphate intermediates that are subsequently reacted with sulfur in 2,6-lutidine to generate phosphate compounds. Oligonucleotide compounds are prepared by treating the phosphate compounds with thiophenoxide (1:2:2 thiophenol/triethylamine/tetrahydrofuran, room temperature, 1 hr). The reaction sequence is repeated until an oligonucleotide compound of the desired length has been prepared. The compounds are cleaved from the support by treating with ammonium hydroxide at room temperature for 1 hr and then are further deprotected by heating at about 50°C overnight to yield preferred antisense compounds.

Selection of antisense compositions specific for a given gene sequence is based upon analysis of the chosen target sequence and determination of secondary structure, T_m, binding energy, relative stability, and antisense compositions were selected based upon their relative inability to form dimers, hairpins, or other secondary structures that would reduce or prohibit specific binding to the target mRNA in a host cell. Highly preferred target regions of the mRNA, are those that are at or near the AUG translation initiation codon, and those sequences that were substantially complementary to 5′ regions of the mRNA. These secondary structure analyses and target site selection considerations were performed using v.4 of the OLIGO primer analysis software (Rychlik, 1997) and the BLASTN 2.0.5 algorithm software (Altschul *et al.,* 1997).

4.29 EXEMPLARY DEFINITIONS

In accordance with the present invention, polynucleotides, nucleic acid segments, nucleic acid sequences, and the like, include, but are not limited to, DNAs (including and not limited to genomic or extragenomic DNAs), genes, peptide nucleic acids (PNAs) RNAs (including, but not limited to, rRNAs, mRNAs and tRNAs), nucleosides, and suitable nucleic acid segments either obtained from native sources, chemically synthesized, modified, or otherwise prepared in whole or in part by the hand of man.

Unless defined otherwise, all technical and scientific terms used herein have the same meaning as commonly understood by one of ordinary skill in the art to which this invention belongs. Although any methods and compositions similar or equivalent to those described herein can be used in the practice or testing of the present invention, the preferred methods and compositions are described herein. For purposes of the present invention, the following terms are defined below:

A, an: In accordance with long standing patent law convention, the words "a" and "an" when used in this application, including the claims, denotes "one or more".

Expression: The combination of intracellular processes, including transcription and translation undergone by a polynucleotide such as, for example, a structural gene to synthesize the encoded peptide or polypeptide.

Promoter: a term used to generally describe the region or regions of a nucleic acid sequence that regulates transcription.

Regulatory Element: a term used to generally describe the region or regions of a nucleic acid sequence that regulates transcription.

Structural gene: A gene or sequence region that is expressed to produce an encoded peptide or polypeptide.

Transformation: A process of introducing an exogenous polynucleotide sequence (*e.g.*, a vector, a recombinant DNA or RNA molecule) into a host cell or protoplast in which that exogenous nucleic acid segment is incorporated into at least a first chromosome or is capable of autonomous replication within the transformed host cell. Transfection, electroporation, and naked nucleic acid uptake all represent examples of techniques used to transform a host cell with one or more polynucleotides.

Transformed cell: A host cell whose nucleic acid complement has been altered by the introduction of one or more exogenous polynucleotides into that cell.

Transgenic cell: Any cell derived or regenerated from a transformed cell or derived from a transgenic cell, or from the progeny or offspring of any generation of such a transformed host cell.

Vector: A nucleic acid molecule (typically comprised of DNA) capable of replication in a host cell and/or to which another nucleic acid segment can be operatively linked so as to bring about replication of the attached segment. A plasmid, cosmid, or a virus is an exemplary vector.

The terms "substantially corresponds to", "substantially homologous", or "substantial identity" as used herein denotes a characteristic of a nucleic acid or an amino acid sequence, wherein a selected nucleic acid or amino acid sequence has at least about 70 or about 75 percent sequence identity as compared to a selected reference nucleic acid or amino acid sequence. More typically, the selected sequence and the reference sequence will have at least about 76, 77, 78, 79, 80, 81, 82, 83, 84 or even 85 percent sequence identity, and more preferably at least about 86, 87, 88, 89, 90, 91, 92, 93, 94, or 95 percent sequence identity. More preferably still, highly homologous sequences often share greater than at least about 96, 97, 98, or 99 percent sequence identity between the selected sequence and the reference sequence to which it was compared. The percentage of sequence identity may be calculated over the entire length of the sequences to be compared, or may be calculated by excluding small deletions or additions which total less than about 25 percent or so of the chosen reference sequence. The reference sequence may be a subset of a larger sequence, such as a portion of a gene or flanking sequence, or a repetitive portion of a chromosome. However, in the case of sequence homology of two or more polynucleotide sequences, the reference sequence will typically comprise at least about 18-25 nucleotides, more typically at least about 26 to 35 nucleotides, and even more typically at least about 40, 50, 60, 70, 80, 90, or even 100 or so nucleotides. Desirably, which highly homologous fragments are desired, the extent of percent identity between the two sequences will be at least about 80%, preferably at least about 85%, and more preferably about 90% or 95% or higher, as readily determined by one or more of the sequence comparison algorithms well-known to those of skill in the art, such as e.*g.*, the FASTA program analysis described by Pearson and Lipman (1988).

The term "naturally occurring" as used herein as applied to an object refers to the fact that an object can be found in nature. For example, a polypeptide or polynucleotide sequence that is present in an organism (including viruses) that can be isolated from a source in nature and which has not been intentionally modified by the hand of man in a laboratory is naturally-occurring. As used herein, laboratory strains of rodents that may have been selectively bred according to classical genetics are considered naturally occurring animals.

As used herein, a "heterologous" is defined in relation to a predetermined referenced gene sequence. For example, with respect to a structural gene sequence, a heterologous promoter is defined as a promoter which does not naturally occur adjacent to the referenced structural gene, but which is positioned by laboratory manipulation. Likewise, a heterologous gene or nucleic acid segment is defined as a gene or segment that does not naturally occur adjacent to the referenced promoter and/or enhancer elements.

"Transcriptional regulatory element" refers to a polynucleotide sequence that activates transcription alone or in combination with one or more other nucleic acid sequences. A transcriptional regulatory element can, for example, comprise one or more promoters, one or more response elements, one or more negative regulatory elements, and/or one or more enhancers.

As used herein, a "transcription factor recognition site" and a "transcription factor binding site" refer to a polynucleotide sequence(s) or sequence motif(s) which are identified as being sites for the sequence-specific interaction of one or more transcription factors, frequently taking the form of direct protein-DNA binding. Typically, transcription factor binding sites can be identified by DNA footprinting, gel mobility shift assays, and the like, and/or can be predicted on the basis of known consensus sequence motifs, or by other methods known to those of skill in the art.

As used herein, the term "operably linked" refers to a linkage of two or more polynucleotides or two or more nucleic acid sequences in a functional relationship. A nucleic acid is "operably linked" when it is placed into a functional relationship with another nucleic acid sequence. For instance, a promoter or enhancer is operably linked to a coding sequence if it affects the transcription of the coding sequence. Operably linked means that the DNA sequences being linked are typically contiguous and, where necessary to join two protein coding regions, contiguous and in reading frame. However, since enhancers generally function when separated from the promoter by several kilobases and intronic sequences may be of variable lengths, some polynucleotide elements may be operably linked but not contiguous.

"Transcriptional unit" refers to a polynucleotide sequence that comprises at least a first structural gene operably linked to at least a first *cis*-acting promoter sequence and optionally linked operably to one or more other *cis*-acting nucleic acid sequences necessary for efficient transcription of the structural gene sequences, and at least a first distal regulatory element as may be required for the appropriate tissue-specific and developmental transcription of the structural gene sequence operably positioned under the control of the promoter and/or enhancer elements, as well as any additional *cis* sequences that are necessary for efficient transcription and translation (*e.g.*, polyadenylation site(s), mRNA stability controlling sequence(s), *etc.*

The term "substantially complementary," when used to define either amino acid or nucleic acid sequences, means that a particular subject sequence, for example, an oligonucleotide sequence, is substantially complementary to all or a portion of the selected sequence, and thus will specifically bind to a portion of an mRNA encoding the selected sequence. As such, typically the sequences will be highly complementary to the mRNA "target" sequence, and will have no more than 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10 base mismatches throughout the complementary portion of the sequence. In many instances, it may be desirable for the sequences to be exact matches, *i.e.* be completely complementary to the sequence to which the oligonucleotide specifically binds, and therefore have zero mismatches along the complementary stretch. As such, highly complementary sequences will typically bind quite

specifically to the target sequence region of the mRNA and will therefore be highly efficient in reducing, and/or even inhibiting the translation of the target mRNA sequence into polypeptide product.

Substantially complementary oligonucleotide sequences will be greater than about 80 percent complementary (or '% exact-match') to the corresponding mRNA target sequence to which the oligonucleotide specifically binds, and will, more preferably be greater than about 85 percent complementary to the corresponding mRNA target sequence to which the oligonucleotide specifically binds. In certain aspects, as described above, it will be desirable to have even more substantially complementary oligonucleotide sequences for use in the practice of the invention, and in such instances, the oligonucleotide sequences will be greater than about 90 percent complementary to the corresponding mRNA target sequence to which the oligonucleotide specifically binds, and may in certain embodiments be greater than about 95 percent complementary to the corresponding mRNA target sequence to which the oligonucleotide specifically binds, and even up to and including 96%, 97%, 98%, 99%, and even 100% exact match complementary to all or a portion of the target mRNA to which the designed oligonucleotide specifically binds.

Percent similarity or percent complementary of any of the disclosed sequences may be determined, for example, by comparing sequence information using the GAP computer program, version 6.0, available from the University of Wisconsin Genetics Computer Group (UWGCG). The GAP program utilizes the alignment method of Needleman and Wunsch (1970). Briefly, the GAP program defines similarity as the number of aligned symbols (*i.e.*, nucleotides or amino acids) that are similar, divided by the total number of symbols in the shorter of the two sequences. The preferred default parameters for the GAP program include: (1) a unary comparison matrix (containing a value of 1 for identities and 0 for non-identities) for nucleotides, and the weighted comparison matrix of Gribskov and Burgess (1986), (2) a penalty of 3.0 for each gap and an additional 0.10 penalty for each symbol in each gap; and (3) no penalty for end gaps.

5.0 EXAMPLES

The following examples are included to demonstrate preferred embodiments of the invention. It should be appreciated by those of skill in the art that the techniques disclosed in the examples which follow represent techniques discovered by the inventor to function well in the practice of the invention, and thus can be considered to constitute preferred modes for its practice. However, those of skill in the art should, in light of the present disclosure, appreciate that many changes can be made in the specific embodiments which are disclosed and still obtain a like or similar result without departing from the spirit and scope of the invention.

5.1 EXAMPLE 1 – INSULATED HERPESVIRUS-DERIVED GENE EXPRESSION CASSETTE FOR SUSTAINED AND REGULATABLE GENE EXPRESSION

This example describes the use of DNA elements derived/isolated from Herpes Simplex Virus type I (HSV-I) in the construction of a gene expression cassette capable of facilitating persistent/long-term and regulatable transgene expression. A novel and enabling feature of this invention is that the cassette is bounded by control elements that protect and insulate the gene expression portion of the cassette from the influence of DNA and chromatin structure that lie outside of the cassette, when the cassette is inserted into a viral vector, cellular, animal or human genome. These control elements effectively maintain the expression cassette in an accessible and transcriptionally-responsive conformation. This novel cassette therefore would allow predictable and sustained [permanent regulatable expression (PRE)] OR [silencing-resistant] expression of a transgene regardless of where the cassette was inserted in a viral vector or a host genome. A key feature of this expression cassette is that it prevents transcription of a gene in a viral vector or transgene from being shut down with time due to chromatin effects of the surrounding DNA. Solving this transcriptional shut-down problem greatly extends the application of existing viral vector and gene delivery technologies.

An integral part of this invention is the expression cassette (FIG. 1), and the novel and key features are the insulating elements that bound the cassette and protect the elements between them from silencing effects of the surrounding chromatin (FIG. 2). As mentioned, this cassette has applications in viral vector, transgenics and other gene delivery applications. The initial embodiment of the invention may be examined in the context of an HSV-1 gene therapy vector construct. Note that, while in this particular embodiment will direct expression from this cassette in a neuron-specific manner, key control elements such as the promoter and enhancer could be replaced with similar elements conferring different tissue/cell-type specificities without altering the PRE properties of the insulating elements.

5.1.1 EXPRESSION CASSETTE-LAT INSULATOR/BOUNDARY 1 (I/B 1) ELEMENT, PROMOTER(S), LAT ENHANCER, HETEROLOGOUS GENE(S), LAT INSULATOR/BOUNDARY 2 (I/B 2) ELEMENT (FIG. 1)

The components of the expression cassette invention consist of a LAT insulator/boundary 1 (I/B1) element, a promoter, the LAT enhancer region flanked by splice donor and splice acceptor sites, a heterologous transgene, and a LAT insulator/boundary 2 (I/B 2) element linked together in that order. The order of the constructs components serves to facilitate permanent and regulatable (in the case of inducible promoter(s)) gene expression. The term "permanent regulatable expression" is taken to mean expression of a heterologous gene(s) from the invention construct for the duration of the host-cell(s) life.

5.1.1.1 LAT INSULATOR/BOUNDARY 1 (I/B 1) ELEMENT

The LAT insulator/boundary 1 (I/B 1) element is defined here as the region comprising HSV1 nucleotides 8,365-9,273 (GenBank NC 001806 : from SwaI-AatII sites), fragments or derivatives of this region, including homologous regions from other alphaherpesviruses that may confer alternative regulation, but are capable of conferring permanent regulatable expression of heterologous genes in the expression cassette comprising the invention.

5.1.1.2 PROMOTERS

A promoter refers to any transcriptional promoter that corresponds to a region of DNA involved in binding of RNA polymerase to initiate transcription. This region of DNA may range in size and complexity from minimal promoters to promoters including upstream activating sequences and enhancers/silencer elements. Within the context of the initial embodiment of this invention, the promoter consists of the HSV-1 latency active promoter 1 (LAP1) comprising nucleotides 117,938-118,843 (GenBank NC 001806 : from SmaI-SacII sites) or pHB22F nucleotides 1,173-2,013 (Berthomme *et al.*, 2000). This promoter allows neuronal-specific expression. Other promoters with different cell-type/tissue specificity could be employed, as well as ones capable of regulation.

5.1.1.3 LAT ENHANCER

An enhancer element refers to any *cis*-acting sequence that increases the utilization eukaryotic transcriptional promoters. Enhancers can function in either orientation and in any location (upstream or downstream) relative to the promoter. Within the context of the invention, the LAT enhancer consists of the HSV-1 sequence corresponding to the LAT 5' exon and comprises from about nucleotide 118,975 to about nucleotide 120,471 (GenBank Accession No. NC_001806) or pHB22F nucleotides 2,050-3,546 (Berthomme *et al.*, 2000). Other enhancers with different cell/tissue-specific or expression properties could also be substituted.

5.1.1.4 HETEROLGOUS GENES

The term heterologous gene comprises any gene other than genes found present within the delivery vector encompassing the expression cassette. The term gene refers collectively to any nucleic acid sequence that is capable of being transcribed and therefore includes sequences encoding mRNA, tRNA, and rRNA. With respect to the growing field of RNAi, the sequence may be in the sense or antisense orientation to the promoter and used to inhibit a target host cell gene. On the other hand, sequences encoding mRNA may include either 5' and/or 3' untranslated regions, transcription stop signals, polyadenylation signals, and/or downstream enhancer/silencer elements. The heterologous

gene may encode a polypeptide for therapeutic use or for use in developing animal models of human disease. Additionally, the heterologous gene may encode antigenic polypeptides for use in vaccine development, the gene may encode a marker gene like green fluorescent protein, or the gene may encode polypeptides that function in the regulation of other genes.

5.1.1.5 LAT INSULATOR/BOUNDARY 2 (I/B 2) ELEMENT

The LAT insulator/boundary 2 (I/B 2) element is defined here as the region comprising HSV1 nucleotides 120,208-120,940 (GenBank NC_001806: PCR fragment tagged with *Spe*I and *Not*I respectively), fragments or derivatives of this region, including homologous regions from other alphaherpesviruses that may confer alternative regulation, but are capable of conferring permanent regulatable expression of heterologous genes in the expression cassette comprising the invention.

5.2 EXAMPLE 2 – WIDE VARIATIONS IN HERPES SIMPLEX VIRUS TYPE 1 INOCULUM DOSE AND LATENCY-ASSOCIATED TRANSCRIPT EXPRESSION PHENOTYPE DO NOT ALTER THE ESTABLISHMENT OF LATENCY IN THE RABBIT EYE MODEL

The latency-associated transcript (LAT) is required for efficient reactivation of herpes simplex virus type 1 from latent infection in the rabbit eye model, but LAT's mechanism of action is unknown. In addition to reactivation, the LAT region seems to correspond to multiple functions, with some LAT deletion mutants exhibiting increased virulence, increased neuronal death and restricted establishment of latency. While a LAT promoter deletion mutant (17ΔPst) seems to be primarily restricted in reactivation in the rabbit, subtle effects on virulence or the establishment of latency cannot be precluded at the normal high levels of virus inoculum used in the rabbit model. Since such additional LAT phenotypes may be more evident with lower doses of virus, the influence of initial viral inoculum and LAT expression on the progression of acute infection and the establishment of latency was evaluated. Both virus recovery rates and viral genome loads in rabbit corneas and trigeminal ganglia have been assayed. Results show that (i) in the corneas and trigeminal ganglia, the maximum amount of virus present during acute infection is independent of the LAT genotype and inoculum dose, although greater viral yields are obtained earlier with higher inoculum doses, and (ii) the range in numbers of latent genomes detected in the ganglia is independent of the inoculum dose and the LAT genotype and therefore no difference in establishment of latency is observed.

Herpes simplex virus type 1 (HSV-1) establishes latency in neurons of sensory ganglia innervating the site of initial infection. The virus can reactivate spontaneously or under conditions of stress to cause a recurrent infection. During latency, the genome forms an episome in neuronal nuclei from which no viral replication occurs (Mellerick and Fraser, 1987; Rock and Fraser, 1983). Approximately one-third of the latently infected neurons express high levels of a single transcript,

termed the latency-associated transcript (LAT) (Gressens and Martin, 1994; Mehta *et al.*, 1995). This transcript is important for reactivation, even though LAT does not seem to encode a protein (Hill *et al.*, 1990; Leib *et al.*, 1989).

While LAT is required for efficient reactivation in animal models, its mechanism is not well understood. One factor that complicates these analyses is that observations vary depending on the animal model (Perug *et al.*, 2001) and the HSV strain (Mitchell *et al.*, 2003; Sawtell *et al.*, 1998) used. The two most common models employed are the rabbit and mouse. In the rabbit eye model, latency is established in trigeminal ganglia (TG) following corneal inoculation. Reactivation, either spontaneous or induced by iontophoresis of epinephrine, is scored by recovery of infectious virus in the tear film (Berman and Hill, 1985; Hill *et al.*, 1986; Nesburn *et al.*, 1967). In the mouse model, latency is established in the trigeminal or dorsal root ganglia following inoculation of corneas or rear footpads, respectively. Viral reactivation from ganglia can be induced by thermal stress, as demonstrated by the presence of infectious virus in the ganglia, or by explant cocultivation of dissected ganglia on cultured cells (Sawtell and Thompson, 1992b; Stevens and Cook, 1971).

Mutants with large LAT deletions have been reported to have reduced numbers of latent viral genomes in neurons of both mice and rabbits (Perng *et al.*, 2000a; Perng *et al.*, 2000b; Sawtell and Thompson, 1992a; Thompson and Sawtell, 2001). This suggests that functions corresponding to the LAT region are involved in the establishment of latency. In contrast, mutants with smaller LAT deletions, such as 17ΔPst (a LAT promoter mutant) and 17Δ348 (a 5' exon deletion mutant), do not demonstrate significant differences in total numbers of latent HSV-1 genomes (Bloom *et al.*, 1994; Bloom *et al.*, 1996; Devi-Rao *et al.*, 1994. This suggests that either the establishment function in the LAT region maps to a region independent of the LAT promoter (LAP1) or that a defect in establishment exhibited by the mutants with smaller deletions was below the limit of detection in the previous studies.

The possibility existed that the dose of virus used in rabbit infections, which involve a relatively large inoculum (1×10^5 to 5×10^5 PFU/eye), may mask subtle replication or establishment deficits inherent in these LAT mutants. Therefore, the course of the acute infection in the rabbit eye model was examined using 1,000-fold-lower inoculation doses of 17ΔPst and the corresponding rescue strain. Differences in acute infection kinetics and levels of establishment of latency were not detected by this method. The observation that peak establishment occurs with even low-dose inocula suggests that saturation of latent sites occurs relatively early. To determine the contribution of the initial inoculum to establishment, rabbits were infected with a nonreplicating HSV-1 recombinant, KD6 ($ICP4^-$). While this recombinant is capable of establishing latency in the rabbit TG following ocular infection, the total number of latent genomes is much lower than that seen after infection with wild-type virus, indicating that peripheral replication contributes to maximal establishment of latency.

5.2.1 MATERIALS AND METHODS

5.2.1.1 CELLS AND VIRUSES

Virus was propagated on cultured rabbit skin (RS) cells. Titers of viral stocks were determined on RS cells grown in minimal essential medium supplemented with 5% fetal bovine serum and antibiotics (Tran *et al.*, 2002). Acute infection titers in eye swabs, corneas and TG were determined on primary rabbit kidney cells grown in minimal essential medium supplemented with 7% fetal bovine serum and antibiotics (Hill *et al.*, 1998). The following HSV-1 genotypes previously described were used in these experiments: wild-type strain 17*syn*+; 17ΔPst, a recombinant with a 202-bp portion of the LAT promoter (nucleotides 118,664 to 118,866) deleted, and the corresponding rescue strain, 17ΔPstR (Devi-Rao *et al.*, 1994); 17Δ348, a LAT recombinant with bases 119,007 to 119,355 deleted, and the corresponding rescue strain, 17Δ348R (Bloom *et al.*, 1996); RHA-6, a recombinant expressing the 5' portion of LAT by virtue of having nucleotides 120,290 to 120,467 removed and replaced with a 442-bp fragment of simian virus 40 encoding the cleavage-polyadenylation signal site (Bloom *et al.*, 1996); and KD6, a recombinant in which both copies of the ICP4 coding sequence have been deleted to yield a nonreplicating virus (Dobson *et al.*, 1990). The KD6 stocks were propagated on complementing E5 cells (DeLuca *et al.*, 1985), and the number of $ICP4^+$ revertants was determined by passage and titration on RS cells (nonpermissive for $ICP4^-$ mutants). All stocks used in this study had less than one revertant per 10^6 PFU of $ICP4^-$ plaques.

5.2.1.2 INFECTIONS

Lightly scarified rabbit eyes were inoculated with the indicated number of PFU in 25-µl aliquots. Rabbits were sacrificed between 1 and 7 days postinfection (dpi) for acute studies, and their corneas and TG were harvested. Latently infected TG were recovered from rabbits 40 dpi. All data presented in individual Tables 5 to 7 and FIG. 3A, FIG. 3B and FIG. 3C are results from separate and independent experiments, each performed on groups of rabbits that were infected and analyzed at the same time.

5.2.1.3 DNA EXTRACTION

Dissected corneas or ganglia were incubated with 0.6 ml of extraction buffer (25 mM EDTA, 100 mM NaCl, 1% sodium dodecyl sulfate, 10 mM Tris [pH 7.5]) and 50 µl of proteinase K solution (15 mg/ml) overnight at 48°C. DNA was extracted three times with phenol-chloroform (1:1) and once with chloroform. DNA was precipitated with ethanol overnight and pelleted by centrifugation. The pellet was washed once with 70% ethanol, air dried, and dissolved in 200 µl of water.

5.2.1.4 ANALYSIS OF THE RELATIVE AMOUNTS OF VIRAL DNA BY PCR™

Semiquantitative PCR™ analysis incorporating [α-^{32}P]dCTP is able to detect 1 pg of purified HSV-1 DNA by comparison to a control plasmid containing a subcloned fragment of the VP5 gene. When purified viral DNA was mixed with uninfected ganglia, fewer than 1,000 viral genomes could be detected. This PCR™ method was also able to detect the viral DNA from a single infected cell. Actin gene primer sets were used to amplify DNA corresponding to cellular genomes to normalize product intensities. The signals were determined by densitometry, and the ratios were calculated (Bloom *et al.*, 1994).

Amplification by PCR™ was carried out as previously described (Bloom *et al.*, 1994) by using the primer sets illustrated in Table 4 for the actin and HSV-1 VP5 genes. The products were radiolabeled for autoradiography and image quantitation by addition of 0.2 μCi of [α-^{32}P]dCTP. The reactions were carried out in an M. J. Research thermal cycler as follows: denaturation, 94°C for 30 sec; annealing, 55°C for 30 sec; and extension, 72°C for 60 sec. The final cycle was terminated with a 10-min extension step. For each reaction, 20 μl (10%) of the DNA sample was used and the final volume of the reaction mixture was 100 μl. One-fifth of the amplified product (corresponding to 2% of the original material) was fractionated on 6% polyacrylamide gels in Tris-borate-EDTA buffer. The PCR™ signals were visualized by scanning an appropriately exposed autoradiogram using a Deskcan II scanner (Hewlett-Packard). The signals were quantified by densitometry using IP Lab Gel software (Signal Analysis Corporation) in accordance with operational instructions.

5.2.1.5 PCR ANALYSIS TO DETERMINE RELATIVE LEVELS OF LATENT VIRAL DNA AND WILD-TYPE REVERTANTS

For these experiments, PCR™ primers specific for the HSV-1 DNA polymerase gene were used to quantitate latent HSV-1 genomes, and the cellular actin gene served as an internal standard for normalizing levels of latent viral DNA among samples. PCR™ primers specific for the HSV-1 ICP4 gene (Table 4) were also used for analysis of the KD6 viral recombinant to confirm that the HSV-1 genomes detected were not due to wild-type revertants. PCRs were performed in a 50-μl final volume consisting of 40.5 μl of sterile H_2O, 1 μl each of both forward and reverse primers (600 ng/μl), 1 μl of deoxynucleoside triphosphates (1.25 mM each), 5 μl of 10× AS buffer [Tris-Cl, KCl, $(NH_4)_2SO_4$, 15 mM $MgCl_2$ (pH 8.7); Qiagen], 1 μl of respective DNA sample, and 0.5 μl of HotStar *Taq* DNA polymerase (5 U/μl; Qiagen). The amplification profile consisted of a step at 95°C for 15 min to activate the *Taq*, followed by one cycle of 94, 55 and 72°C for 3 min, followed by 30 identical cycles of 1 min each (Ericomp Twinblock System, Easy Cycler). PCR™ products were resolved on 5% polyacrylamide gels, stained with SYBR Green (Molecular Probes), and scanned with a Storm

PhosphorImager (Molecular Dynamics) using a 450-nm-wavelength laser. Relative numbers of latent genomes were determined by establishing the ratio of HSV-1 polymerase product to cellular actin within each sample. Viral polymerase-specific PCR™ products were compared to a plasmid titration mixture containing the subcloned target sequence spiked into processed, uninfected rabbit TG tissue. The signal intensity of each sample was compared to that of this titration mixture to determine the relative number of latent HSV-1 molecules in each sample. Dilutions (twofold) of all samples were performed to determine the appropriate amount of sample yielding a linear response and falling within the linear range of the standard curve.

TABLE 4
PCR™ PRIMERS

Gene Target	Primer Pair	Product Size (bp)
HSV-1 VP5 gene	5'-TGAACCCCAGCCCCAGAAACC-3' (SEQ ID NO:1) 5'-CGAGTAAACCATGTTAAGGACC-3' (SEQ ID NO: 2)	149
HSV-1 ICP4 gene	5'-CTGATCACGCGGCTGCTGTACACC-3' (SEQ ID NO:3) 5'-GGTGATGAAGGAGCTGCTGTTGCG-3' (SEQ ID NO: 4)	144
HSV-1 DNA polymerase gene	5'-CATCACCGACCCGGAGAGC-3' (SEQ ID NO:5) 5'-GGGCCAGGCGCTTGTTGGTGTA-3' (SEQ ID NO:6)	92
Rabbit actin gene	5'-AAGATCTGGCACCACACCTT-3' (SEQ ID NO:7) 5'-CGAACATGATCTGGGTCATC-3' (SEQ ID NO:8)	110

5.2.1.6 STATISTICAL ANALYSES

Results in Tables 2, 3 and 4 were analyzed using factorial analyses of variance with within-subject (nesting of tissue and virus strain combinations within an animal) arrangement of treatments. Post hoc evaluation of means following a significant overall model fit and significant interactions was conducted using protected *t* tests and a simulation method to correct alpha levels for the number of comparisons carried out (Edwards and Berry, 1987).

TABLE 5

RELATIVE AMOUNTS OF VIRAL DNA (EXPRESSED AS THE RATIOS OF VP5 DNA TO ACTIN DNA) AT A HIGH DOSE OF INOCULATION (500,000 PFU)[a]

dpi	Mean value ± SEM in corneas for:		Mean value ± SEM in ganglia for:	
	17ΔPst	17ΔPstR	17ΔPst	17ΔPstR
1	1.51 ± 0.54	1.19 ± 0.99	0.12 ± 0.12	0.23 ± 0.19
2	2.29 ± 0.76	1.40 ± 0.94	0.65 ± 0.26	0.37 ± 0.28
3	2.11 ± 0.32	2.38 ± 0.59	1.10 ± 0.26	1.86 ± 0.66
5	2.31 ± 0.64	1.59 ± 0.18	1.80 ± 0.36	1.74 ± 0.39
7	2.16 ± 1.30	2.01 ± 0.27	0.80 ± 0.20	0.54 ± 0.40

14	0.44 ± 0.14	0.36 ± 0.34	0.43 ± 0.30	0.21 ± 0.23

[a]Rabbits' eyes were inoculated with 500,000 PFU of 17ΔPst or 17ΔPstR (rescue strain). At the indicated times postinfection, the rabbits (two rabbits per virus per time point) were sacrificed and corneas (four per virus per time point) and TG (four per virus per time point) were dissected. Total DNA was isolated from the tissue and amplified with VP5 and actin gene primer sets in combination. The relative amounts of viral DNA (ratios of VP5 DNA to actin DNA) were determined by densitometry.

TABLE 6
RELATIVE AMOUNTS OF VIRAL DNA IN CORNEAS AND TG DURING ACUTE INFECTIONS FOLLOWING LOW-DOSE INOCULATION WITH VIRUSES OF DIFFERENT LAT GENETYPES[a]

Virus	dpi	Mean value ± SEM[b] in: Corneas	Ganglia
17*syn*+	1	0.21 ± 0.12	0.03 ± 0.01
	2	0.82 ± 0.55	0.03 ± 0.02
	3	0.88 ± 0.46	0.07 ± 0.04
	5	0.79 ± 0.87	0.49 ± 0.48
	7	1.42 ± 0.49	0.50 ± 0.31
	21	0.22 ± 0.09	0.22 ± 0.13
17ΔPst	1	0.27 ± 0.16	0.03 ± 0.30
	2	0.37 ± 0.24	0.08 ± 0.30
	3	0.51 ± 0.36	0.05 ± 0.30
	5	1.44 ± 0.56	0.39 ± 0.30
	7	0.83 ± 0.79	0.16 ± 0.30
	21	0.30 ± 0.23	0.25 ± 0.31
17Δ348	1	0.40 ± 0.28	0.04 ± 0.04
	2	0.23 ± 0.22	0.03 ± 0.04
	3	0.36 ± 0.27	0.03 ± 0.04
	5	0.80 ± 0.55	0.31 ± 0.04
	7	0.83 ± 0.70	0.21 ± 0.21
	21	0.23 ± 0.12	0.28 ± 0.21
17Δ348R	1	0.30 ± 0.33	0.03 ± 0.01
	2	0.59 ± 0.47	0.03 ± 0.01
	3	0.92 ± 0.67	0.17 ± 0.35
	5	1.83 ± 0.69	0.61 ± 0.42
	7	1.83 ± 1.45	0.74 ± 0.70
	21	0.22 ± 0.10	0.22 ± 0.01
RHA-6	1	0.10 ± 0.13	0.04 ± 0.03
	2	0.07 ± 0.09	0.03 ± 0.02
	3	0.67 ± 0.35	0.07 ± 0.04
	5	1.20 ± 0.35	0.46 ± 0.34
	7	0.79 ± 0.65	0.57 ± 0.34
	21	0.15 ± 0.11	0.33 ± 0.15

[a] Rabbit eyes were inoculated with 500 PFU of 17*syn*+, 17ΔPst, 17Δ348, 17Δ348R, and RHA-6. At the indicated dpi, corneas and TG (four each per virus per time point) were dissected and the relative amounts of viral DNA were determined.

[b] Relative amounts of viral DNA are presented as the ratios of the HSV VP5 gene to the cellular

Virus	dpi	Mean value ± SEM[b] in: Corneas	Ganglia

actin gene as determined by PCR™. Means and standard errors of the mean (SEM) are presented as least-squares mean values and were calculated as described above.

TABLE 7
RELATIVE AMOUNTS OF VIRAL DNA PRESENT IN TG DURING LATENCY IN RABBITS INFECTED WITH DIFFERENT DOSES OF VIRUS[a]

Virus, dose	Rabbit tattoo no. (left or right TG)[b]	HSV-1 DNA (mean no. of genome equivalents)	Amt. of viral DNA (mean ± SEM)[c]
17ΔPst, 500 PFU	A3 (L)	30,000	18,300 ± 7,888
	A3 (R)	2,000	
	A5 (L)	40,000	
	A5 (R)	1,200	
17ΔPstR (rescue strain), 500 PFU	A9 (L)	800	12,200 ± 7,888
	A9 (R)	8,000	
	A10 (L)	30,000	
	A10 (R)	10,000	
17ΔPst, 50,000 PFU	A26 (L)	1,200	10,750 ± 7,888
	A26 (R)	1,800	
	A30 (L)	3,000	
	A30 (R)	11,000	
17ΔPstR (rescue strain), 50,000 PFU	A31 (L)	8,000	16,500 ± 7,888
	A31(R)	3,000	
	A32 (L)	15,000	
	A32 (R)	40,000	

[a] Rabbits were inoculated with the indicated doses of 17ΔPstR or 17ΔPst in both eyes. Total DNA was isolated from latently infected ganglia (40 dpi) and analyzed by PCR™ amplification with actin and VP5 gene primer sets. Data are from four TG per dose per virus per time point.
[b] L, left; R, right.
[c] Relative amounts of viral DNA are expressed as the number of genome equivalents of HSV determined following semiquantitative PCR™ for the HSV DNA polymerase gene and are standardized to the amount of cellular actin present in each sample. Standard curves were generated using known amounts of HSV polymerase target DNA in order to calculate the number of genomes present in each sample. Means and standard errors of the mean (SEM) were calculated as described above.

5.2.2 RESULTS

5.2.2.1 ACUTE REPLICATION IN RABBIT CORNEAS AND TG IN HIGH- VERSUS LOW-DOSE INFECTIONS

The contributions of both LAT expression and inoculation dose were analyzed over the course of acute ocular infection of rabbits with either 500 or 500,000 PFU of 17ΔPst or 17ΔPstR (rescue strain)/eye. Infectious virus yields during the acute infection were measured in tear swabs, corneas and TG (FIG. 3A, FIG. 3B and FIG. 3C). At high viral doses (5×10^5 PFU), titers were highest in the tears

and corneas on the first dpi. These levels tended to reach a lower plateau by days 3 through 7, and the virus was undetectable by day 14. Virus titers in TG increased during the first 3 days of infection, followed by 3 days (days 3 to 7 postinfection) of sustained virus titers, with the peak occurring during this period. As in the case of the corneas, virus was not detectable by day 14. Infection of rabbits with an inoculum of 500 PFU resulted in the detection of less infectious virus in the eye swabs and corneas at 1 and 2 dpi. However, by day 3, the amounts of infectious virus present in these samples were indistinguishable from those in the samples from rabbits infected with 5×10^5 PFU (FIG. 1A and FIG. 1B). A similar lag was evident in the ability to detect infectious virus in TG of rabbits receiving the 500-PFU inoculum (FIG. 1C), and it was not until days 5 to 7 that TG from rabbits infected with 500 PFU of each virus contained amounts of infectious virus similar to those contained in the TG from rabbits infected with 5×10^5 PFU. When the replication curves of the two different viruses, 17ΔPst and 17ΔPstR, were compared, they were roughly colinear and not significantly different for either the eye swabs, corneas or TG. So, while the infecting dose clearly affected the initial infection kinetics, it did not significantly alter maximal virus yields. In addition, the ability to express LAT had no identifiable effects on acute replication in the eyes or TG.

5.2.2.2 ANALYSIS OF VIRAL DNA LEVELS IN CORNEAS AND TG DURING ACUTE INFECTION

While the use of 1,000-fold-lower inoculum doses of 17ΔPst and its rescue strain did not identify any differences in viral yields during the acute infection, the possibility remained that there might be detectable differences in genome loads. PCR™ analysis to determine the relative amounts of viral DNA present in corneas and TG following both high-dose (5×10^5 PFU per eye) and low-dose (500 PFU per eye) infection was performed. The relative amounts of viral DNA present in corneas and TG following high-dose infection did not show significant differences based on LAT genotypes at any time points (Table 5). The course of infection was then examined following a much lower dose infection (500 PFU per eye). In general, the amounts of HSV-1 DNA detected in the corneas versus those detected in the TG paralleled the findings from infectious virus assays. As with the high-titer infections, relative amounts of HSV-1 DNA in corneas were greater than those in TG during the entire acute infection course (Table 6). Comparison of the data in Tables 5 and 6 revealed a delay in the increases in viral DNA in the lower-dose infections, and the peak values for viral DNA occurred at the same time points as in the infectious virus assays (FIG. 3A, FIG. 3B and FIG. 3C). Since the assay results for viral DNA seemed to parallel the data obtained for infectious virus and also permitted the detection of viral genomes as the virus entered latency, several different LAT mutations were evaluated in a low-dose infection by using this method of analysis. In addition to the LAT promoter deletion recombinant, 17ΔPst, the recombinants 17Δ348, its rescue strain, and RHA-6 were included in this analysis. These other two recombinants differ in LAT expression and/or reactivation phenotypes;

17Δ348 expresses LAT but exhibits significant reactivation impairment following epinephrine induction, whereas RHA-6, which contains a simian virus 40 cleavage-polyadenylation sequence in the middle of the 2.0-kb LAT intron, expresses LAT and reactivates normally (Bloom *et al.*, 1994).

Rabbits inoculated with 500 PFU of reactivation-impaired viral recombinants (17Δ348 and 17ΔPst) demonstrated significantly decreased amounts of viral DNA in TG during the acute phase of infection compared to rabbits inoculated with the wild type, 17*syn*+, and RHA-6 (Table 6). At day 5 postinfection, the mean value for the reactivation-impaired mutants (0.35 ± 0.19 [ratio of VP5 DNA to actin DNA]) was marginally significantly different ($P = 0.068$) from that for the normal reactivators (0.56 ± 0.38). Mean values for HSV DNA at day 7 (0.29 ± 0.18 for reactivation-impaired viruses and 0.63 ± 0.31 for normally reactivating viruses) were again significantly different ($P = 0.006$), but by the time the active acute infection had cleared (21 days), all TG values were statistically indistinguishable for all of the viruses tested. Therefore, during the initial phase of the low-dose infection, there was a transient period (days 3 to 7) during which somewhat less viral DNA was detected in the TG following infection with the LAT recombinants containing deletions in the LAT region. As the infection progressed and then resolved (day 21), this difference was no longer seen.

5.2.2.3 THE RELATIVE AMOUNTS OF LATENT VIRAL DNA IN TG OF RABBITS INFECTED WITH THE WILD TYPE OR LAT MUTANTS WERE SIMILAR REGARDLESS OF INFECTING DOSE

The amount of viral DNA in ganglia following clearance of the acute infection suggested that viral genome loads in the ganglia were independent of LAT genotype and infecting dose. This observation was extended to a strict latency time point by using semiquantitative PCR™ to carefully compare relative amounts of latent viral DNA over a range of infecting doses (FIG. 4 and Table 7). Rabbit corneas inoculated with 500 to 50,000 PFU/eye were sacrificed 40 dpi to determine the amount of latent HSV-1. Comparison of 17ΔPst with its rescue strain at an inoculum of 500 PFU resulted in mean numbers of genome equivalents that overlapped when standard error and statistical analyses were applied ($P = 0.94$; least-squares means analysis). A similar comparison of the mean numbers of HSV-1 genome equivalents of these two recombinants following a 50,000-PFU infection indicated that that there was no statistical significance assignable to differences in the latent infections established by 17ΔPst and 17ΔPstR ($P = 0.95$). Next, an analysis of differences in numbers of latent genomes present as a function of infecting inoculum was performed. Comparisons of 17ΔPst at 500 versus 50,000 PFU and 17ΔPstR at 500 versus 50,000 PFU resulted in P values of 0.94 and 0.97, respectively. In summary, no statistical difference in numbers of viral genomes was detected as a function of either LAT genotype or initial virus dose. As with the high-titer infections examined in Table 5, neither dose nor LAT genotype affected DNA levels in latently infected TG.

5.2.2.4 A NONREPLICATING HSV-1 RECOMBINANT ESTABLISHED A LATENT INFECTION IN THE TG BUT AT LOWER LEVELS THAN WILD-TYPE VIRUS

The analysis of the course of the acute infection as a function of dose seemed to indicate that, in the rabbit eye model, the ultimate amount of DNA that established latency in the TG was only a small fraction of the amount that reached the ganglia during the entire course of the acute infection. This result was not surprising; however, comparison of the relative levels of DNA accumulation observed in the high-dose and low-dose infections suggested that a "saturating threshold" of HSV DNA in the ganglia, or the ultimate amount of latent DNA, might actually be reached relatively early during the acute infection. This raised the question as to the relative role that the input inoculum might have on the establishment of a latent infection, particularly the normal high-dose inocula used in the rabbit model. To further assess the contribution of input inoculum versus the need for ocular replication for efficient establishment of latency, a nonreplicating (ICP4$^-$) HSV-1 recombinant (KD6) was used. The amount of HSV-1 DNA was determined by PCR™ using TG from rabbits inoculated with 10^5 or 10^6 PFU of this virus at 14 dpi (FIG. 5). While TG of rabbits inoculated with KD6 contained detectable HSV genomes, overall numbers were lower than those observed using replication-competent HSV-1 strain 17*syn*+. PCR™ analysis of these ganglia (using primers specific for the ICP4 gene) indicated that the DNA present was not due to ICP4 revertants. These results demonstrated that while nonreplicating HSV-1 recombinants could seed the TG and establish a latent infection, replication was required to achieve wild-type levels of establishment. These data also suggested that while a high-dose inoculum can result in a significant amount of HSV-1 DNA in the TG at 1 dpi, much of this DNA (and the DNA that ultimately establishes a latent infection in the rabbit TG) is the product of replication.

5.2.3 DISCUSSION

LAT has been suggested to play a role in protecting neurons from death or apoptosis during the initial stages of establishment (Perng *et al.*, 2000a; Thompson and Sawtell, 2001; Thompson and Sawtell, 2000). These observations have been made with mutants that carry deletions extending from the entire LAT promoter into the 2.0-kb intron and that often display altered virulence. While such effects were never observed with the 202-bp LAT promoter mutant (17ΔPst), the statistical power required for discerning threefold (or less) establishment or virulence defects is difficult to achieve in the rabbit model (Bloom *et al.*, 1994). The goal of this study was to determine whether subtle deficits in replication or establishment were detectable using inocula of 500 and 50,000 PFU, doses that are 10- and 1,000-fold lower than normal 17ΔPst inocula in the rabbit eye model. The hope was that additional multiple rounds of replication permitted by the lower inoculum doses might amplify subtle replicative or establishment defects.

No significant differences in the amounts of infectious virus produced during the acute infection in corneas and ganglia or in the numbers of latent genomes in rabbit TG were observed. A slight, but statistically significant, decrease in DNA accumulation was observed at days 3 to 7 of the acute infection in the case of several of the LAT mutations that are correlated with reactivation defects. The fact that DNA levels in the TG were comparable to those for the normally reactivating viruses at day 21 (and during latency) suggests that this DNA accumulation defect was transient and that 17ΔPst's defect in reactivation in the rabbit eye model was not simply the result of less DNA being present in the ganglia during latency. While statistical analyses cannot rule out the possibility that 17ΔPst may have a very subtle reduction in overall establishment of latency, it is unlikely that a decreased amount of DNA alone is the primary basis of the dramatic restriction in reactivation displayed by LAT mutants.

One possible explanation for not seeing the effect on establishment reported for other LAT deletion mutants is that the other studies have employed recombinants with relatively large deletions (Perng *et al.*, 2000b; Thompson and Sawtell, 2001). The fact that these other deletions encompass not only the LAT promoter but also the 5' exon and part of the intron suggests that the primary effect on establishment observed in these systems may be mediated by a distinct genetic element that lies outside of the 202-bp LAT promoter deletion in 17ΔPst. Previous studies have shown that a promoter element (LAP2) exists downstream of the primary latent LAT promoter and that this promoter is active in acutely infected ganglia (Chen *et al.*, 1995; Goins *et al.*, 1994; Nicosia *et al.*, 1993). It should be pointed out that while the LAP1 deletion in 17ΔPst eliminates almost all latent LAT expression, transcription from the LAP2 promoter can still be detected in acute ganglia. Therefore, the contribution of this element to the course of the acute and/or establishment phases of infection is not eliminated and may therefore suggest a role for this downstream region in these processes.

Another observation is that lower (and probably more physiologically relevant) doses of viruses are sufficient to efficiently establish latency in the rabbit TG. It is interesting that increasing inoculum does not decrease the scatter in total levels of establishment observed in the rabbit TG over a range of doses. This scatter is likely due to variability in the numbers of nerve termini that are physically accessible to the initial inoculum and local replication of the virus in the cornea. The fact that 17ΔPst and 17PstR show similar wide and overlapping ranges of establishment in the rabbit TG but that 17ΔPst exhibits a 5- to 10-fold reduction in the number of rabbits or eyes that can be adrenergically induced to reactivate (Bloom *et al.*, 1996; Jarman *et al.*, 2002) highlights long-standing observation that, at least in the rabbit, the absolute genome load seems to be secondary to the genotype of the HSV strain in determining the potential for reactivation.

While this suggests that the level of establishment, as measured by the amount of HSV-1 DNA present in the TG during latency, is not the primary defect in 17ΔPst's ability to reactivate, it does not rule out the idea that LAT plays some role in establishment. In fact, it is very possible that 17ΔPst may

be altered in a function that substantially impacts the quality of HSV-1 establishment, such as the efficient regulation of transcription or accessibility of the HSV latent genome, a possibility first suggested by Chen et al. (1997). It is also possible that 17ΔPst alters the establishment program, perhaps resulting in pushing of the HSV latent infection to populations of neurons that are less permissive for induced reactivation. It should be pointed out that the numbers of latently infected neurons, phenotypic distribution, and the numbers of genome copies per neuron have not been analyzed with these mutants in the rabbit. These have been shown to be critical parameters defining the potential to reactivate in the mouse (Sawtell, 1998; Sawtell *et al.*, 1998). Future studies will be required to investigate how these parameters are altered in the case of 17ΔPst.

Another interesting finding was that the amount of HSV-1 DNA detected in the corneas remained high at 21 dpi. While latent-stage (28 dpi or later) corneas from rabbits infected at low doses (such as the day-21 corneas for which results are shown in Table 6) were not examined, a previous study that examined reactivation of LAT^+ viruses versus that of LAT^- viruses in the rabbit model revealed that (i) there were relatively high amounts of HSV DNA detected in the corneas of rabbits infected with 17*syn*+ and the 17ΔPst rescue strain and, interestingly, (ii) there was approximately 10-fold less HSV DNA in the corneas of rabbits infected with the LAT promoter deletion recombinant 17ΔPst. In contrast, no significant differences in amounts of HSV DNA present in the TG from rabbits infected with these three viruses were detected (Devi-Rao *et al.*, 1997). One interpretation of these data is that the presence of HSV-1 DNA in the corneas is actually the result of persistent seeding that is the result of reactivation from the TG and the fact that less 17ΔPst was detected in the corneas at latent-stage times suggests that this virus's decreased ability to reactivate results in substantially less seeding of the corneas. The findings in the present example that there were relatively high (and comparable) amounts of HSV DNA in the corneas of rabbits infected with both LAT^+ and LAT^- viruses at days 14 and 21 suggests that by day 21 the DNA resulting from the acute infection-establishment phase of the latent infection had not yet cleared from the corneas. Indeed, this supports the rationale of waiting until at least 28 dpi for analysis of latency.

This study provided the additional opportunity to monitor the course of an HSV-1 ocular infection in the rabbit as a function of dose. Not surprisingly, peak acute titers in the tears, corneas, and TG were delayed by several days when lower inocula were used. Interestingly, peak levels of viral DNA in the TG were reached slightly earlier, suggesting that maximum establishment of the latent DNA pool occurs fairly early and at relatively low inoculation doses. This in turn suggests that corneas provide a limited number of entry sites into the nervous system (or number of available neuronal termini), which become saturated relatively quickly. To address this question more directly, a nonreplicating virus, KD6, was used (Dobson *et al.*, 1990; Sedarati *et al.*, 1993). Since this virus cannot undergo any replication in the cornea, it allows assessment of the amount of viral DNA delivered to the TG as a direct function of input. Results indicate that while significant establishment

of latency is achieved, even doses of 10^6 PFU yield approximately a 10-fold lower amount of DNA than that seen with a lower inoculum of 17*syn*+. This indicates that while a nonreplicating virus can establish latency in TG, replication is required to establish maximal latent infections. This requirement is likely due to mechanical barriers that must be overcome to efficiently gain access to the nerve termini projecting to the TG. While infecting the corneal surface (even with scarification) provides access to many nerve termini, replication and cell-to-cell spread are much more important factors.

5.3 EXAMPLE 3 – CTCF BINDS SEVERAL CLUSTERS OF CTCF CONSENSUS MOTIFS WITHIN THE HSV-1 GENOME DURING LATENCY

The present example identifies the location of putative boundaries that separate the transcriptionally permissive LAT region, from the surrounding regions of hypoacetylation and transcriptional repression. A previous study had suggested that these boundaries were located within a ~5 kb region both 5' to and 3' to the region of the LAT that is hyperacetylated during latency. These data demonstrate that sequence analysis of these 5' and 3' regions identified clusters of a repeated motif for a cellular protein known as CTCF, a protein known to have a role in the formation of cellular boundaries. These two clusters of CTCF motifs are contained in a region of approximately 250 bp each, one 5' to the LAT promoter, near the RL and UL junctions, and the other in the region encoding the LAT intron. ChIP analysis using an antibody specific for CTCF demonstrated that, during a latent infection of murine dorsal root ganglia (DRG), these two sites are enriched in CTCF, suggesting that these 250 bp elements may contain the core nucleation sites for the formation of a functional chromatin boundary. The formation of such a boundary surrounding the LAT enhancer may play an essential role in insulating the LAT enhancer, which confers activity of the LAT promoter during latency, from acting in a transcriptionally permissive manner on ICP0, or other lytic genes in the region.

Further analysis of the HSV-1 genome revealed the existence of four other clusters of CTCF motifs. ChIP analysis revealed that during a latent infection of murine DRG, these sites are also enriched in CTCF binding. Interestingly, if these motifs all were to form functional boundaries, each of the HSV-1 IE genes would exist in a separate chromatin domain. Finally, analysis of the genomes of other alphaherpesviruses for which sequence is available reveals that these CTCF motifs and their placement flanking IE genes are conserved among this group. This suggests that the organization of the IE genes (and LAT) into separate chromatin domains may be an important regulatory component of the control of alphaherpesviral latent gene expression and may contribute in a mechanistic way to the control of latency and reactivation.

5.3.1 MATERIALS AND METHODS

5.3.1.1 VIRUSES AND CELLS

Sequence analyses were performed using published NCBI GenBank sequence for HSV-1 strain 17 (NC 001806; McGeoch), HSV-2 strain HG52 (NC 001798; McGeoch), Suid herpesvirus 1 (pseudorabies virus) (BK001744; Enquist), Human herpesvirus 3 strain Dumas (varicella-zoster virus) (X04370; Scott), and Cercopithecine herpesvirus 1 (monkey B virus) (NC 004812; Hilliard). All ChIP experiments were performed using a low passage stock of HSV-1 strain 17*syn*+ prepared from a master stock obtained from J. Stevens. The virus was amplified and titrated on rabbit skin cells (RSC) using Eagle's minimal essential medium (MEM, Life Technologies) supplemented with 5% calf serum (Life Technologies) and antibiotics (250 U of penicillin/mL, 250 μg of streptomycin/mL, and 292 μg of L-glutamine/mL).

5.3.1.2 MOUSE INFECTIONS

Four- to six-week old female Out-bred ND4 Swiss mice (Harlan) were anesthetized by Halothane inhalation and pretreated with 0.05 ml of a 10% (wt/vol in water) sterile saline solution injected under each rear footpad. At 3-4 hr after pretreatment, the mice were anesthetized by intramuscular injection of 0.010-0.020 ml of a cocktail of acepromazine (2.5-3.75 mg/kg), xylazine (7.5-11.5 mg/kg) and ketamine (30-45 mg/kg) and infected bilaterally on the rear footpads with 1.5×104 PFU/mouse. The keratinized epithelium was lightly abraded with an emery board, and the inoculum was applied to the feet in a volume of 50 μl/mouse. The inoculum was spread over the surface of the footpad with the side of the pipette tip, and the virus was allowed to adsorb for 30-45 min while the mice remained under anesthesia on their backs. Mice were sacrificed at >28 days p.i. for latent studies. Care was taken to ensure that the ganglia were removed and processed as quickly as possible postmortem (between 3 and 5 min per mouse).

5.3.1.3 IDENTIFICATION OF CONSENSUS CTCF BINDING MOTIFS

The frequency with which CCCTC or CTCCC motifs are found within the HSV-1 genome was calculated by the formulas R = fCCCTC/1000 and R = fCTCCC/1000, where f is the frequency of the indicated CTCF-binding motif, and R is the resulting ratio. The entire viral genome was analyzed as 1000 bp segments using a Visual Basic program, and the results output to Microsoft Excel and graphed. Regions that exhibited high frequencies of motif occurrence were further analyzed for motif clustering (Benson, 1999). Tandem repeat analysis was also applied to a group of alphaherpersviruses to screen for similar CTCF motif clusters.

5.3.1.4 CHROMATIN IMMUNOPRECIPITATION (CHIP)

ChIP assays were performed as previously described (20) with minor modification. Briefly, steps were as follows. All solutions used prior to the collection of chromatin-antibody complexes contained protease inhibitors at the following concentrations: aprotinin (U.S. Biochemicals), 15 μg/ml; leupeptin (U.S. Biochemicals), 1 μg/ml; and phenylmethylsulfonyl fluoride (Sigma), 10 μg/ml. All steps were performed at 4°C unless noted otherwise. DRG were removed from mice at a minimum of 28 days p.i. and homogenized in ice-cold phosphate-buffered saline. Formaldehyde (final concentration, 1% [vol/vol]) was added to the homogenate to cross-link chromatin, and samples were incubated at room temperature for 10 min with shaking. Cross-linking was arrested by adding glycine (0.125 M final concentration), and the homogenate incubated for an additional 5 min at room temperature with shaking. The homogenate was then pelleted, washed 3 times with phosphate-buffered saline, then resuspended in SDS lysis buffer (Upstate Biotechnology) and incubated a minimum of 10 min on ice.

The cell lysate was sonicated to shear the chromatin into a population of fragments with a median size range of 500-1,000 bp as determined by agarose gel electrophoresis. The sheared chromatin was diluted by the addition of 10 volumes of ice-cold ChIP dilution buffer (Upstate Biotechnology) and incubated with salmon sperm DNA-protein A agarose (50%) slurry (Upstate Biotechnology) for 2 hr to reduce non-specific binding. Beads were removed by centrifugation and sheared chromatin incubated with 2 μL of anti-CTCF (Upstate Biotechnology) at a concentration of 2 μg/mL of antibody per 1 mL pre-cleared chromatin overnight with shaking.

Chromatin-antibody complexes were collected by incubation with salmon sperm DNA-protein A-agarose (50%) slurry and subsequent collection of beads by centrifugation. Bead pellets were washed one time each in low-salt, high-salt, and LiCl immune complex wash buffers followed by two washes with TE buffer (all Upstate Biotechnology). Antibody-chromatin complexes were eluted from beads by incubation with freshly made, preheated (65°C) elution buffer (0.1% SDS, 0.1M $NaHCO_3$). NaCl was added to eluates (final concentration of 0.2 M) and they were incubated at 65°C for 4 hr. The eluates were then treated with RNase A and proteinase K, and the DNA was purified using a Qiaquick PCR™ purification kit (Qiagen).

5.3.1.5 PCR™ ANALYSIS OF CHIPS

Following collection of the chromatin-antibody complexes with salmon sperm-protein A agarose beads, the unbound supernatant (subsequently referred to as "input") was removed and purified in a manner similar to the bound ChIP fraction described above. Serial dilutions of input were used as reference in order to determine the relative enrichments of different DNA targets in the bound ChIP

fraction. PCRs on input dilutions and the bound ChIP fraction were performed simultaneously using HotStar Taq (Qiagen) at cycles that produced product within the linear range, which was typically attained between 30-38 cycles. Initial stage PCR™ cycle conditions used were as follows: 15 min at 95°C, 3 min at 94°C, 3 min at 55°C, and 3 min at 72°C. Subsequent, repeated cycles were as follows: 1 min at 94°C, 1 min at 55°C, and 1 min at 72°C (repeated 30-38 times). PCR™ primers used for ChIP analysis are listed in Table 8.

TABLE 8
PCR™ PRIMERS

DNA Target	Sequence	Product Size (bp)	Accession No. (nucleotide no.)
Mouse *Tsix* Site A[a]	5'-GGAGCCTAAACCTGTCTGTC-3' (forward) (SEQ ID NO:9) 5'-GTGTGTCATAGCTCAAGAGG-3' (reverse) (SEQ ID NO:10)	139	AJ421479 (137291 - 137430)
Mouse MT498[a]	5'-ACTCAGTCCAAACATATACAAGATGC-3' (forward) (SEQ ID NO:11) 5'-CTATCTACAACAAACTTCTCCTGGG-3' (reverse) (SEQ ID NO:12)	185 or 149[b]	NT_039554 (1203018 - 1203201)
HSV-1 CT1	5'-GCATGCGTCGCCCAAC-3' (forward) (SEQ ID NO:13) 5'-CAGTTAGATTGCATGTGATC-3' (reverse) (SEQ ID NO:14)	89	NC_001806 (117067 - 117156)
HSV-1 CT2	5'-CTCTGTGGTTAACACCAGAG-3' (forward) (SEQ ID NO:15) 5'-GTCTGTCTTGGATGTATCGC-3' (reverse) (SEQ ID NO:16)	204	NC_001806 (120461 - 120665)
HSV-1 CT4/5	5'-CAACGCTACTGCAAAAC-3' (forward) (SEQ ID NO:17) 5'-GACGGGGTGCTGTAAC-3' (reverse) (SEQ ID NO:18)	97	NC_001806 (127149 - 127426)
HSV-1 CT6	5'-CACGAACGACGGGAGCG-3' (forward) (SEQ ID NO:19) 5'-CACCCAAGGTGCTTACC-3' (reverse) (SEQ ID NO:20)	248	NC_001806 (132140 - 132388)
HSV-1 CT7	5'-CGTGATCGCCTGTCTCC-3' (forward) (SEQ ID NO:21) 5'-CATTGCCAATCGAACCC-3' (reverse) (SEQ ID NO:22)	179	NC_001806 (143513 - 143692)
HSV-1 gC	5'-CCTTGCCGTGGTCCTGTGGA-3' (forward) (SEQ ID NO:23) 5'-GTTGGGGTTTGGGGTCGATG-3' (reverse)	186	NC_001806 (96331 - 96517)

DNA Target	Sequence	Product Size (bp)	Accession No. (nucleotide no.)
	(SEQ ID NO:24)		

[a] Chao *et al.*, 2002.
[b] The MT498 locus is polymorphic within the amplicon.

All PCR™ products were resolved on 7.5% polyacrylamide gels, stained with SYBR Green (Molecular Probes) and detected using a Storm 860 Fluorimager (Molecular Dynamics). Band intensities for each PCR™ product were determined using ImageQuant Software V1.2. For data shown in Table 9, band intensities for input samples were graphed, a linear regression applied, and an equation for the line determined, all using Kaleidegraph software. The equation for the line was used to determine the total relative enrichment of the PCR™ products generated using the same primer set on DNA from the precipitated (bound) ChIP fraction. The enrichment of one DNA region over another in a given bound ChIP fraction was determined by comparing the relative enrichment quantity obtained for two DNA regions of interest. These comparisons yield fold difference of enrichment of one DNA target over another by dividing the larger relative enrichment value by the smaller relative enrichment value. In all cases, the immunoprecipitated samples were compared with serial dilutions of the input, and mean values and standard deviations were calculated.

TABLE 9

PCR™ DETERMINATION OF THE RELATIVE ENRICHMENT OF CTCF AT IDENTIFIED CTCF MOTIF CLUSTERS FOLLOWING CHIP

Panel[a]	PCR™ Primers	Experiment No.[b]	Sample, No. of Cycles	Dilution[c]	Fluorescence[d]	IP Value[e]	Mean ± SD IP Value
A	*Tsix* Site A		Input, 36	0.01	2.319×10^6		
				0.005	1.766×10^6		
				0.0025	1.171×10^6		
		1	IP, 36	0.1	1.575×10^6	0.004	
		2	IP, 36	0.1	1.174×10^6	0.003	0.003 ± 0.001
		3	IP, 36	0.1	6.967×10^5	0.002	
	MT498		Input, 35	0.01	2.219×10^6		
				0.005	1.159×10^6		
				0.0025	7.199×10^5		
		1	IP, 35	0.1	8.159×10^5	0.003	
		2	IP, 35	0.1	2.298×10^5	0.002	0.002 ± 0.001
		3	IP, 35	0.1	2.418×10^5	0.002	
B	CT1		Input, 38	0.1	2.998×10^6		
				0.05	1.565×10^6		
				0.025	4.192×10^5		

Panel[a]	PCR™ Primers	Experiment No.[b]	Sample, No. of Cycles	Dilution[c]	Fluorescence[d]	IP Value[e]	Mean ± SD IP Value
		1	IP, 38	0.1	1.801×10^6	0.046	
		2	IP, 38	0.1	5.505×10^5	0.027	0.071 ± 0.060
		3	IP, 38	0.1	2.981×10^6	0.139	
	CT4/5		Input, 35	0.1	1.1162×10^6		
				0.05	4.7241×10^5		
				0.025	2.4803×10^5		
		1	IP, 35	0.1	6.4805×10^5	0.046	
		2	IP, 35	0.1	1.9476×10^4	0.022	0.056 ± 0.040
		3	IP, 35	0.1	1.7140×10^6	>0.1	
	CT6		Input, 38	0.1	6.2552×10^5		
				0.05	3.6653×10^5		
				0.025	1.5552×10^5		
		1	IP, 38	0.1	1.1460×10^6	>0.1	
		2	IP, 38	0.1	1.5976×10^5	0.026	0.075 ± 0.043
		3	IP, 38	0.1	2.0132×10^6	>0.1	
	CT7		Input, 33	0.1	7.8063×10^5		
				0.05	2.8792×10^5		
				0.025	2.2306×10^4		
		1	IP, 33	0.1	9.0591×10^5	>0.1	
		2	IP, 33	0.1	4.2321×10^5	0.041	0.080 ± 0.034
		3	IP, 33	0.1	1.5675×10^6	>0.1	
	gC		Input, 33	0.1	4.578×10^5		
				0.05	2.961×10^5		
				0.025	8.640×10^4		
		1	IP, 33	0.1	1.268×10^5	0.028	
		2	IP, 33	0.1	4.110×10^4	0.023	0.028 ± 0.006
		3	IP, 33	0.1	2.129×10^5	0.034	
C	CT2		Input, 35	0.1	3.003×10^5		
				0.05	1.869×10^5		
				0.025	1.300×10^5		
		1	IP, 35	0.01	6.408×10^4	0.02	
		2	IP, 35	0.01	1.175×10^5	0.025	0.025 ± 0.006
		3	IP, 35	0.01	1.566×10^5	0.031	
	gC		Input, 34	0.1	8.234×10^5		
				0.05	5.124×10^5		
				0.025	3.956×10^5		
		1	IP, 34	0.01	8.610×10^4	0.016	
		2	IP, 34	0.01	9.404×10^4	0.017	0.017 ± 0.001
		3	IP, 34	0.01	1.727×10^5	0.018	

Panel[a]	PCR™ Primers	Experiment No.[b]	Sample, No. of Cycles	Dilution[c]	Fluorescence[d]	IP Value[e]	Mean ± SD IP Value

[a] Samples included either input (mock-immunoprecipitated) or IP (immunoprecipitated with anti-CTCF) samples that were analyzed by PCR™. Values reflect quantitations of FIG. 7A, FIG. 7B and FIG. 7C samples.

[b] ChiP analyses were conducted using samples processed from three independent experiments.

[c] Input and IP samples were serially diluted as indicated.

[d] PCR™ products were resolved by polyacrylamide gel electrophoresis and stained with SYBR green. The band intensities were imaged on a Storm 860 instrument and measured using ImageQuant software.

[e] The data from input dilutions were fit by linear regression (Kaleidagraph). The IP fluorescence value was calculated from the linear fit of the input dilution data.

5.3.2 RESULTS

5.3.2.1 THE HSV-1 GENOME CONTAINS CLUSTERS OF BINDING MOTIFS FOR THE CELLULAR PROTEIN CTCF

Previous studies indicated that a region of the latent HSV-1 genome encompassing the LAT promoter and extending through the region encoding the LAT 5' exon is significantly enriched in the specifically modified histone H3 acetyla (K9, K14), whereas the ICP0 promoter, and UL54 are under-enriched in this histone. This suggested that chromatin boundaries might be present to separate these regions of differing transcriptional permissivity and histone composition. The resolution of the previous study focused attention on the 5-kb region upstream of the LAT promoter, and a similar 5-kb region downstream of the region encoding the LAT 5' exon. Upon examination of the sequence in these regions, clusters of two different consensus motifs (5'CTCCC3' and 5'CCCTC3') were identified for the cellular protein CTCF in these regions surrounding the hyperacetylated portion of the LAT locus. The HSV-1 genome contains clustered CTCF binding sites. An algorithm that searched for CCCTC or CTCCC motifs was used to analyze the HSV-1 genome in 1000-bp segments to determine the frequency with which these CTCF binding sites occur in the positive (direct) and negative (complement) DNA strands. Sequence analysis of the identified segments containing a high frequency of motifs reveals a clustering of the CTCF motifs. What is interesting to note is that these clusters contain multiple copies of the CTCF motifs, and that these motifs are periodically separated by intervening sequences (FIGS. 6A and 6B). For example, the cluster (CT2) that is located within the region encoding the LAT intron (FIG. 6B) contains 9 copies of the CTCF motif "CTCCC" separated by 8 reiterations of the sequence "ACGCACCCCCA" (SEQ ID NO:25). The cluster (CT1) located upstream of the LAT promoter, near the UL/RL junction possesses a slightly different arrangement (FIG. 6A) with 23 copies of the CTCF motif "CTCCC" interspersed by alternating reiterations of "CT" and "CCCT." In addition, the CT1 cluster also contains 22 copies of the alternate CTCF motif

"CCCTC" that are interleaved within the same sequence containing the CTCCC motif. For this reason in FIGS. 6A-6B, the reiteration of a single repeat motif has been depicted as a triangle (as in CT2), and the cluster containing the interleaved "double motifs" as a double triangle (CT1).

TABLE 10

Motif	Sequence
CT1	5'-TAACTGGCTCCCCTCTCCCCCCTCTCCCCTCTCCCCCCTCTCCCCTCTCCCCCCCTCTC CCCTCTCCCCCCCCTCTCCCCTCTCCCCCCCCTCTCCCCTCTCCCCCCCTCTCCCCTCTCCCCC CCTCTCCCCTCTCCCCCCCCTCTCCCCTCTCCCCCCCCTCTCCCCTCTCCCCCCCCTCTCCCCTC TCCCCCCCCTCTCCCCTCTGCTCTTT-3' (SEQ ID NO:26)
CT2	5'-CTCTGTGGTTAACACCAGAGCCTGCCCAACATAGGCCCCCCACTCCCACGCACCCCCAC TCCCACGCACCCCCACTCCCACGCACCCCCACTCCCACGCACCCCCACTCCCACGCACCCCC ACTCCCACGCACCCCCACTCCCACGCACCCCCACTCCCACGCACCCCCACTCCCACGCATCC CCGCGATACATCCAACACAGAC-3' (SEQ ID NO:27)
CT3	5'-CGGCGTCTGGCCGCTCCTCCCCCCGCTCCTCCCCCCGCTCCTCCCCCCGCTCCTCCCCC CGCTCCTCCCCCCCGCTCCTCCCCCCCGCTCCTCCCCCCCGCTCCTCCCCCCCGCTCCTCCCCCGC TCCTCCCCCCCGCTCCTCCCCCCCGCTCCTCCCCCCCGCTCCTCCCCCCCGCTCCTCCCCCCCGCTC CTCCCCCCCGCTCCTCCCCCCCGCTCCTCCCCCCCGCTCCTCCCCCCCGCTCCCGCGGCC-3' (SEQ ID NO:28)
CT4/5	5'-CACCACCGCCCCCTCCCCAGCCCCAGCCCTCCCCAGCCCCAGCCCTCCCCGGCCCCAGC CCTCCCCGGCCCCAGCCCTCCCCGGCCCCAGCCCTCCCCGGCCCCAGCCCTCCCCGGCCCCA GCCCTCCCCGGCCCCAGCCCTCCCCGGCGCGTCCCGCGCTCCCTCGGGGGGGTTCGGGCATC TCTACCTCAGTGCCGCCAATCTCAGGTCAGAGATCCAAACCCTCCGGGGGCGCCCGCGCACC ACCACCGCCCCTCGCCCCCTCCCGCCCCTCGCCCCCTCCCGCCCCTCGCCCCCTCCCGCCCC TCGCCCCCTCCCGCCCCTCGCCCCCTCCCGCCCCTCGCCCCCTCCCGCCCCTCGCCCCCTCC CGCCCCTCGCCCCCTCCCGCCCCTCGCCCCCTCCCGCCCCTCGCCCCCTCCCGCCCCTCGCC CCCTCCCGCCCCTCGCCCCCTCCCGCCCCTCGCCCCCTCCCGCCCCTCGCCCCCTCCCGCCC CTCGCCCCCTCCCGCCCCTCGCCCCCTCCCGCCCCTCGCCCCCTCCCGCCCCTCGCCCCCTC CCGCCCCTCGCCCCCTCCCGCCCCTC-3' (SEQ ID NO:29)
CT6	3'-CTCCCCCCCTGCGCCCCCGCCTCCTCCCCCCTGCGCCCCCGCCTCCTCCCCCCTGCGCC CCCGCCTCCTCCCCCTGCGCCCCCGCCTCCTCCCCCCTGCGCCCCCGCCTCCTCCC-5' (SEQ ID NO:30)
CT7	3'-CCCTCACCCACCCACCCCTCACCCACCCACCCCTCACCCACCCACCCCTCACCCACCCA CCCCTCACCCACCCACCCCTCACCCACCCACCCCTCACCCACCCACCCCTCACCCACCCACC CCTCACCCACCCACCCCTC-5' (SEQ ID NO:31)

Additional analysis of both strands of the HSV-1 genome using a motif searching algorithm identified 4 other significant clusters of these two motifs in the HSV-1 genome (FIGS. 6A-6B). These are CT3 (located within the "a" sequence region), CT4/5 (located within the RS regions at that the 3' end of the coding region for ICP4), CT6 (located in the RS regions, 5' to the ICP4 promoter) and CT7 (located within the US near the US/RS junction). As depicted in FIGS. 6A-6B, some of these CT clusters contain reiterations of only a single type of CTCF motif, as in the case of CT2 (CT3, CT6, and CT7), while CT4/5 contains 51 reiterations of the CCCTC motif, and 29 copies of the CTCCC motif interleaved. The clustered motifs are present on both strands of the genome, and possess a striking symmetry when viewed on a linear depiction of the genome and when viewed on a circular depiction, it can be seen that these CT clusters organize the HSV-1 genome into 11 separate domains. In this

arrangement, each of the IE genes, as well as the 5' end of LAT, are contained within a separate domain compartment.

5.3.2.2 ChIP Analysis Reveals That the CT Clusters are Enriched in CTCF During Latency

Since sequence analysis revealed that the HSV-1 genome contains clustered CTCF motifs, it was sought to determine whether the cellular protein CTCF binds these clusters during latency. Chromatin immunoprecipitation (ChIP) analysis was performed on chromatin extracted from the DRG of mice latently infected with HSV-1 strain 17*syn*+. Dilutions of input DNA were subjected to PCR™ with each respective primer set to serve as controls for relative primer efficiencies. Furthermore, Input dilutions served as a reference for determining the relative enrichment of CTCF within the IP samples at the various target DNA clusters. To validate the ChIP, PCR™ primers for regions of the mouse genome that had been shown to be positive (*Tsix*) and negative (MT498) for CTCF binding were employed (Lee *et al.*). ChIP analysis of three independent ChIP experiments revealed significant enrichment of CTCF at the *Tsix* locus (FIG. 7A) when compared to the MT498 negative control, consistent with a previous report (Lee *et al.*). This validation provided a basis for the analysis and comparison of CTCF binding at specific viral regions. PCR™ primers specific for the various identified CTCF motif clusters were used to screen the same three IP samples for CTCF binding (FIG. 7B and FIG. 7C). As with the cellular controls, the viral CTCF clusters show significant enrichment of CTCF as opposed to the glycoprotein C (gC) region, which does not contain CTCF motif clusters. Due to the proximity and limited resolution of ChIP analysis with sonicated chromatin (500-1000 bp) PCR™ analysis was performed with primers to the CT4/5 region but may not be able to distinguish between enrichment at the CT3 region since there is less than 700-bp difference between these clusters. Nevertheless, enrichment of CTCF at the motif clusters within the HSV-1 latent genome is comparable to, and often exceeds, the enrichment seen with the cellular controls.

5.3.2.3 Clusters of CTCF Motifs are Conserved Among Other Alphaherpesviruses

If the clusters of CTCF motifs identified in HSV-1 play an important role in establishing chromatin boundaries in a manner that regulates latent and lytic gene transcription, one might expect these motifs to be conserved among the alphaherpesviruses. In order to investigate this hypothesis, CTCF motif analysis was performed on the genomic sequence of several other alphaherpesviruses for which sequence was available. As depicted in FIGS. 8A-8E, clusters of CTCF motifs were identified in all of the viruses analyzed, including HSV-2 strain HG-52, Cercopithecine herpesvirus 1 (Herpesvirus simiae or B-virus), varicella zoster virus (VZV) strain Dumas and Pseudorabies virus (PrV). Even though several of these viruses contained an alternative CTCF motif (CCCGC, CGCCC,

CCCTG, or GTCCC) (Table 11), the striking feature is that these motifs all occurred in tandem clusters, and in a similar configuration as observed in HSV-1. Specifically, the repeats are situated in such a manner that each of the immediate early genes are bounded by a pair of these clusters (when the genome is viewed in a circular configuration). Taken together, these data indicate the clustering of these sequence motifs is highly conserved evolutionarily across even relatively distinct members of the alphaherpesvirus family.

TABLE 11

Virus	Cluster No.	Cluster Nucleotide Position	Putative Insulator Motif Sequence (Repeat Motif Sequence)	SEQ ID NO:
HSV-1	1	98-320	GGAGCGGGGGGA	SEQ ID NO:32
	2	988-1040	CCCCCGCGA	SEQ ID NO:33
	3	5726-5877	GGGGGTGCGTGGGAGT	SEQ ID NO:34
	4	9032-9212	GGGGAGAGGGGAGAGGG	SEQ ID NO:35
	5	71605-71814	TGGGGC	SEQ ID NO:36
	6	117158-117340	CTCCCCTCTCCCCCCCT	SEQ ID NO:37
	7	120494-120645	GCACCCCCACTCCCAC	SEQ ID NO:38
	8	125331-125383	CGCGGGGGT	SEQ ID NO:39
	9	126051-126273	CCGCTCCTCCCC	SEQ ID NO:40
	10	126571-126709	CCCTCCCCGGCCCCAG	SEQ ID NO:41
	11	126810-127142	CCGCCCCTCGCCCCCTC	SEQ ID NO:42
	12	132388-132513	GGGCGGAGGAGGGGGGACGCGG	SEQ ID NO:43
	13	143712-143864	TGGGTGGGTGGGGAG	SEQ ID NO:44
	14	145676-145845	CCCCCTCCTCCGCCCCCGCGTC	SEQ ID NO:45
	15	151091-151423	CGAGGGGCGGGAGGGGG	SEQ ID NO:46
	16	151524-151662	GCCGGGGAGGGCTGGG	SEQ ID NO:47
	17	151960-152128	GGAGCGGGGGGA	SEQ ID NO:48
HSV-2	1	444-546	CCCGCCGCCGGGGTC	SEQ ID NO:49
	2	943-1070	CCCCTCCGACCCCCTGACG	SEQ ID NO:50
	3	4653-4770	CCGCCTCCTCCTCCT	SEQ ID NO:51
	4	9043-9193	CGCGCGGCGGCCGGGCGGGGG	SEQ ID NO:52
	5	72098-72266	GGCAGGGGCGGCTGG	SEQ ID NO:53
	6	106045-106165	CCTCCCGCC	SEQ ID NO:54
	7	118057-118207	GCGCGCCCCCGCCCGGCCGCC	SEQ ID NO:55
	8	123643-123779	GCCCGACCCCC	SEQ ID NO:56
	9	126180-126307	GGGGGTCGGAGGGGCGTCA	SEQ ID NO:57
	10	126766-126806	CCGGCGGCGGGGACC	SEQ ID NO:58

Virus	Cluster No.	Cluster Nucleotide Position	Putative Insulator Motif Sequence (Repeat Motif Sequence)	SEQ ID NO:
	11	127466-127490	CCCGCGGCCGCCTCC	SEQ ID NO:59
	12	127672-127914	CCGCCCGCCCGACCC	SEQ ID NO:60
	13	133227-133644	CCGGGGGGACGGG	SEQ ID NO:61
	14	144419-144448	CCCCCCCGTCG	SEQ ID NO:62
	15	148097-148366	CCCCGTCC	SEQ ID NO:63
	16	158828-154070	CGGGGGTCGGGCGGG	SEQ ID NO:64
	17	154252-154287	CGCGGGGGAGGCGGC	SEQ ID NO:65
Herpes B virus	1	119-156	CCGGGAGCCCGC	SEQ ID NO:66
	2	1289-1356	GCGGGCGGTCC	SEQ ID NO:67
	3	3548-3634	GCCCAGGCCCGC	SEQ ID NO:68
	4	3658-3738	GCCCGGCGCCCAAGTCCC	SEQ ID NO:69
	5	5164-5245	CCAGAAGCAGAGAGGGGCGGGGGCTCC	SEQ ID NO:70
	6	5247-5367	GGAGAAGCACAAGACCCACACACGCGCG GCAGGGGCACGGAGGCGGGGGGAGGCCC GGGA	SEQ ID NO:71
	7	6057-6167	AGGGGGGCGAGGGGA	SEQ ID NO:72
	8	43039-43135	GGGGGTGCGGGGGCGGT	SEQ ID NO:73
	9	71555-71764	GGGCAGCAG	SEQ ID NO:74
	10	115968-116247	CCTCCCCTCCCCCGCGCCCC	SEQ ID NO:75
	11	119694-119796	CCTTCCCCTCGCCCG	SEQ ID NO:76
	12	120491-120611	CTCCCGGGCCTCCCCCCGCCTCCGTGCCC CTGCCGCGCGTGTGTGGGTCTCGGGCTTC TC	SEQ ID NO:77
	13	120613-120694	GGGAGCCCCCGCCCCTCTCTGCTTCTG	SEQ ID NO:78
	14	124502-124569	GCGGACCGCCC	SEQ ID NO:79
	15	125702-125739	GGGCGGGCTCCC	SEQ ID NO:80
	16	125966-126051	CTCCCGTCCCC	SEQ ID NO:81
	17	133423-133805	CCCCGCGCACCCCTCGCCCTCCCCTC	SEQ ID NO:82
	18	139332-139450	CCACCCCCGCCCCCACCA	SEQ ID NO:83
	19	148619-149001	GGGCGAGGGGTGCGCGGGGGAGGGGA	SEQ ID NO:84
	20	156373-156458	GGGAGGGGGAC	SEQ ID NO:85
	21	156685-156722	CCGGGAGCCCGC	SEQ ID NO:86
Pseudo-rabies	1	746-963	CCTTTCCCCCAACCCCCTCGTTCCCC	SEQ ID NO:87
	2	2320-2682	GGGGAGATGGGGAGAGGAGAT	SEQ ID NO:88

Virus	Cluster No.	Cluster Nucleotide Position	Putative Insulator Motif Sequence (Repeat Motif Sequence)	SEQ ID NO:
	3	16212-16802	GGGACGGAGGGGAGA	SEQ ID NO:89
	4	32674-32879	CCCCAAGTCC	SEQ ID NO:90
	5	50181-50276	GGGACGGCGGG	SEQ ID NO:91
	6	63110-63319	CGCCCTCTCTCCCAC	SEQ ID NO:92
	7	63388-63459	AAGGGGTCTCT	SEQ ID NO:93
	8	80325-80545	TGGGGGAGAGGA	SEQ ID NO:94
	9	95518-95623	GGGGGGAGTCT	SEQ ID NO:95
	10	101376-101501	GCATAACCCCTCCCCCTAATCT	SEQ ID NO:96
	11	108490-108688	TGTGGTGGTCTCTGTGTTG	SEQ ID NO:97
	12	117279-117687	GGGGTGGAGACGGTGGAGGGAGAGGGG AGTGGGAT	SEQ ID NO:98
	13	117752-117841	GGGGGAGTCC	SEQ ID NO:99
	14	126761-126850	GGACTCCCCC	SEQ ID NO:100
	15	126915-127323	CTCTCCCTCCACCGTCTCCACCCCATCCC ACTCCC	SEQ ID NO:101
	16	135914-136112	ACCACCACACAACACAGAG	SEQ ID NO:102
	17	143101-143226	GGGGGAGGGGTTATGCAGATTA	SEQ ID NO:103
Varicella	1	13953-14208	GAGGGAGAGGCGGAG	SEQ ID NO:104
	2	20692-21017	GCGGGATCGGGCTTTCGGGAAGCGGCCG AGGTGGGCGCGACG	SEQ ID NO:105
	3	41453-41519	GCCCGCGCA	SEQ ID NO:106
	4	109762-109907	CCCCGCCGATGGGGAGGGGGCGCGGTA	SEQ ID NO:107
	5	119990-120135	CATCGGCGGGGTACCGCGCCCCCTCCC	SEQ ID NO:108

5.4 EXAMPLE 4 – DEVELOPMENT OF HSV-1 INSULATOR CASSETTE

To demonstrate that the HSV-1 Insulator Cassette (containing B1 and B2) is capable of maintaining sustained expression of a reporter gene in the context of a gutted HSV-1 vector (Insulated Viral Artificial Chromosome or *IVAC*), the test vectors (and a control vector lacking the insulators) may be delivered to mouse dorsal root ganglia. Quantitative analysis of the transgene expression as a function of time (*e.g.*, 4, 14, 21, 40, 80, 160, 320 days, *etc.*) may then be used as an indication of the effectiveness of the disclosed constructs.

To demonstrate that the insulation cassette works in the context of a transgenic animal (*e.g.*, a transgenic mouse) following insertion into cellular chromosomes, populations of transgenic mice may be created (as well as a control group that lacks the insulation cassette). Assessment of tissue-specific

expression may be determined as well as analysis of changes in the surrounding chromatin profile (*e.g.*, by ChIP using antibodies specific for different histone modifications) to assess ability of insulator to protect surrounding chromatin from effects of the enhancer contained within the cassette. Quantitative analysis of the transgene expression as a function of time (*e.g.*, 4, 14, 21, 40, 80, 160, 320 days) in a number of individual founders (taking into account different sites of integration) may also be used as an indication of the effectiveness of the disclosed constructs.

To further characterize functional properties of B1 and B2 and to identify proteins involved in function, analysis of enhancer-blocking properties of B1 as well as cell-type specific characteristics of B1 and B2 may be performed using transient assays. Likewise, yeast-one hybrid analysis of regions to the left and right of the CT elements may be examined to identify cellular proteins that confer: 1) insulation properties, 2) enhancer-blocking properties, as well as 3) cell-type specific properties. In a similar fashion, yeast-two hybrid analyses may be performed of regions to the left and right of the CT elements to identify cellular proteins that confer: 1) insulation properties, 2) enhancer-blocking properties; and as well 3) cell-type specific properties, in combination with CTCF binding.

5.5 EXAMPLE 5 – SEQUENCE OF EXEMPLARY HUMAN HERPESVIRUS GENOMES

Examples of illustrative human Herpesvirus genomes from which insulator cassette sequences may be obtained for use in practice of the present invention are illustrated in SEQ ID NO: 109, SEQ ID NO:110, and SEQ ID NO:11 in the accompanying sequence listing. While no means an exhaustive list, the sequences of human herpesvirus 1, 2, and 3 are representative of the viral genomes from which the insulator sequences of the present invention may be obtained.

SEQ ID NO:109 Human Herpesvirus 1 (GenBank Accession No. NC_001806)

SEQ ID NO:110 Human Herpesvirus 2 (GenBank Accession No. NC_001798)

SEQ ID NO:111 Human Herpesvirus 3 (GenBank Accession No. NC_001348)

6.0 REFERENCES

The following references, to the extent that they provide exemplary procedural or other details supplementary to those set forth herein, are specifically incorporated herein by reference.

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All of the compositions and methods disclosed and claimed herein can be made and executed without undue experimentation in light of the present disclosure. While the compositions and methods of this invention have been described in terms of preferred embodiments, it will be apparent to those of skill in the art that variations may be applied to the compositions and methods and in the steps or in the sequence of steps of the method described herein without departing from the concept, spirit and scope of the invention. More specifically, it will be apparent that certain agents which are both chemically and physiologically related may be substituted for the agents described herein while the same or similar results would be achieved. All such similar substitutes and modifications apparent to those skilled in the art are deemed to be within the spirit, scope and concept of the invention as defined by the appended claims.